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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 83.3%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GGAAGTCTTTTCTTTTCTTTTCTTTT 4483
1 GTAGCTTTTCTTTTCTTTTCTTTTCTTTT 24

RESULT 942
LOCUS AU264231 26 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264231 VS Dictyostelium discoideum cDNA VSD54 5', mRNA
SEQUENCE
AU264231
AU264231.1 GI:20523029
EST.
Dictyostelium discoideum
Dictyostelium discoideum
ORGANISM
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 26)
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
Unpublished (2002)
JOURNAL
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobio1.tsukuba.ac.jp.
LOCATION/Qualifiers
1..26
/organism="Dictyostelium discoideum"
/mol type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD54"
/sex="mat A"
/dev stage="vegetative"
/clone_lib="VS"

FEATURES
source

Query Match
Best Local Similarity 80.0%; Score 17.6; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5473 TTTTGTAAAGTAATTTTGT 5497
1 TTTTGTAAAGTAATTTTGT 5497

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DB 25 TTTTGTATGATGATTAATTTTGT 1

RESULT 943
LOCUS CF302323 26 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-L19, b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-L19, mRNA sequence.
ACCESSION CF302323
VERSION CF302323.1 GI:33674084
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gsbdo.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
1..26
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-L19"
/tissue type="leaf"
/dev stage="7 days after germination"
/lab host="E. coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 83.3%; Score 17.6; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTT 24

RESULT 944
LOCUS AZ422541 26 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0201614F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0201614 F, genomic survey sequence.
ACCESSION AZ422541
VERSION AZ422541.1 GI:10546554
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
Contact: Robert B. Weiss

```

University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddum@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0201 row: G column: 14  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers

## FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UDGCM0201G14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UDGCM library"
/notice="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 17.6; DB 1; Length 26;  
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4468 TTTTCTTTTCTTCTGAG 4481  
 Db 1 TGTCTTTTCTTCTGAG 24

RESULT 945  
 EX550767 27 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX550767 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse114f12\_p1c, mRNA sequence.  
 ACCESSION BX550767  
 VERSION BX550767.1 GI:33374306  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

## AUTHORS

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

## TITLE

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942  
 PUBMED 14519198

## COMMENT

Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.  
 Location/Qualifiers

## FEATURES

source

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1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/notice="country: Zimbabwe; EST from adult gut infected with T. brucei"
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Query Match 0.2%; Score 17.6; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 9e+02;  
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Qy 4459 TGGACTTTTCTTTTCTTTT 4482  
 Db 4 TAGATAGTTTCTTTTCTTTT 27

RESULT 946  
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 LOCUS BX550946 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse115f11\_p1c, mRNA sequence.  
 ACCESSION BX550946  
 VERSION BX550946.1 GI:33374735  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

## REFERENCE

1 (bases 1 to 27)

## AUTHORS

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

## TITLE

JOURNAL Genome Biol. 4 (10), R63 (2003)

## MEDLINE

## PUBMED

22881942  
 14519198

## COMMENT

Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.  
 Location/Qualifiers

## FEATURES

source

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/organism="Glossina morsitans morsitans"
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REFERENCE	AUTHORS	TITLE
1 (bases 1 to 27)	Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina</i>

morsitans morsitans and expression analysis of putative immune response genes  
 Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source Location/Qualifiers

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 /issue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 9e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4459 TGGACTTTTCTTTTCTTTTCTTTT 4482  
 Db 4 TAGATAGTTTTTTTCTTTTCTTTT 27

RESULT 950  
 EX551552  
 LOCUS BX551552 27 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX551552 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse119c07\_plc, mRNA sequence.  
 ACCESSION BX551552  
 VERSION BX551552.1 GI:33375771  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)  
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source Location/Qualifiers

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 /organism="Glossina morsitans morsitans"  
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Query Match 0.2%; Score 17.6; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 9e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 951  
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 LOCUS BX551708 27 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX551708 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse11c02\_plc, mRNA sequence.  
 ACCESSION BX551708  
 VERSION BX551708.1 GI:33376038  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 27)  
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

REFERENCE 1 (bases 1 to 27)  
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source Location/Qualifiers

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 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 9e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



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Oy      4459 TCGACTTTTTCCTTTTTTTTTTTT    4482
         ||| | | | | | | | | | | | | | |
Db      4 TAGATAGCTTTTTTTTTTTTTTTTTT    27

RESULT 952
LOCUS   BX551731
DEFINITION BX551731 Glossina morsitans morsitans adult infected gut Glossina
          morsitans morsitans cDNA clone Tseelid03_p1c, mRNA sequence.
ACCESSION BX551731
VERSION   BX551731.1 GI:33376060
KEYWORDS EST.
SOURCE    Glossina morsitans morsitans
           Glossina morsitans morsitans
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
AUTHORS Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
           morsitans morsitans and expression analysis of putative immune
           response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hal N
           Pathogen Sequencing Unit
           The Sanger Institute The Wellcome Trust Genome Campus
           Hinxton, Cambridge, CB10 1SA, UK
           Request for clones, please contact: Mike Lehane
           Prof. M.J.Lehane
           School of Biological Sciences,
           University of Wales,
           Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
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            T.brucei"
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Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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         ||| | | | | | | | | | | | | | |
Db      4 TAGATAGCTTTTTTTTTTTTTTTTTT    27

RESULT 953
LOCUS   BX551875
DEFINITION BX551875 Glossina morsitans morsitans adult infected gut Glossina
          morsitans morsitans cDNA clone Tseil20c06_p1c, mRNA sequence.
ACCESSION BX551875
VERSION   BX551875.1 GI:33376196
KEYWORDS EST.
SOURCE    Glossina morsitans morsitans
           Glossina morsitans morsitans
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorphia;

```

REFERENCE	Hippoboscoidae; Glossiniidae; Glossina.
AUTHORS	1. (bases 1 to 27) Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL	Genome Biol. 4 (10), R63 (2003)
MEDLINE	22881942
PUBMED	14519198
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
FEATURES	location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse120c06.pic" /tissue_type="adult infected gut" /clone_id="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
Query Match	0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity	83.3%; Pred. No. 9e+02; 4; Indels 0; Gaps 0;
Matches	20; Conservative 0; Mismatches 4
4459	4459 TGACATTTTTTTTTTTTTTTTTT 4482
4	4 TAGATGTTTTTTTTTTTTTTTTT 27
RESULT 954	
LOCUS	BX551974 27 bp mRNA linear EST 10-OCT-2003
DEFINITION	BX551974 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse120h2.pic, mRNA sequence.
ACCESSION	BX551974
VERSION	BX551974.1
KEYWORDS	GI:33376288
SOURCE	EST.
ORGANISM	Glossina morsitans morsitans Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.
REFERENCE	1 (bases 1 to 27) Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
AUTHORS	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
TITLE	Genome Biol. 4 (10), R63 (2003)
JOURNAL	22881942
MEDLINE	14519198
PUBMED	14519198
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences,

VERSION BX553159.1 GI:33377351

**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
**REFERENCE** 1 (bases 1 to 27)  
**AUTHORS** Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
**JOURNAL** Genome Biol. 4 (10), R63 (2003)  
**MEDLINE** 22881942  
**PUBMED** 14519198  
**COMMENT** Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.  
**FEATURES**  
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 4 TAGATAGTTTCTTTTCTTTTCTTTT 27

**RESULT** 958  
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**DEFINITION** morsitans morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse128h11\_plc, mRNA sequence.  
 BX553354  
**VERSION** BX553354.1 GI:33377529  
**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 27)  
**AUTHORS** Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
**JOURNAL** Genome Biol. 4 (10), R63 (2003)  
**MEDLINE** 22881942  
**PUBMED** 14519198  
**COMMENT** Contact: Hall N  
 Pathogen Sequencing Unit

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 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.  
**FEATURES**  
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**Query Match** 0.2%; Score 17.6; DB 1; Length 27;  
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 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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**RESULT** 959  
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**LOCUS** BX553476 27 bp mRNA linear EST 10-OCT-2003  
**DEFINITION** BX553476 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse129f12\_plc, mRNA sequence.  
 BX553476  
**VERSION** BX553476.1 GI:33377634  
**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 27)  
**AUTHORS** Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
**JOURNAL** Genome Biol. 4 (10), R63 (2003)  
**MEDLINE** 22881942  
**PUBMED** 14519198  
**COMMENT** Contact: Hall N  
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 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.  
**FEATURES**  
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Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
OY	4459	TGACCTTTT	TTTTTTTTTTT	4482
DB	4	TAGATAGT	TTTTTTTTTTTTT	27
RESULT 960				
LOCUS	BX553666	27 bp	mRNA	linear EST 10-OCT-2003
DEFINITION	BX553666	Glossina morsitans morsitans adult infected gut	Glossina morsitans morsitans cDNA clone Tse12H08_p1c	mRNA sequence.
ACCESSION	BX553666			
VERSION	BX553666.1	GI:33377811		
KEYWORDS	EST.			
SOURCE	Glossina morsitans morsitans			
ORGANISM	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	Lehane, M.J., Akopy, S., Gibson, W., Keshornu, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL MEDLINE PUBMED	Genome Biol. 4 (10), R63 (2003)			
COMMENT	14519198			
	Contact: Hall N			
	Pathogen Sequencing Unit			
	The Sanger Institute The Wellcome Trust Genome Campus			
	Hinxton, Cambridge, CB10 1SA, UK			
	Request for clones, please contact: Mike Lehane			
	Prof. M.J. Lehane			
	School of Biological Sciences,			
	University of Wales,			
	Bangor LL57 2UW			
	All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.			
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	/clone_lib="Glossina morsitans morsitans adult infected gut"			
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Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
OY	4459	TGACCTTTT	TTTTTTTTTTT	4482
DB	4	TAGATAGT	TTTTTTTTTTTTT	27
RESULT 961				
LOCUS	BX553666	27 bp	mRNA	linear EST 10-OCT-2003
DEFINITION	BX553666	Glossina morsitans morsitans adult infected gut	Glossina morsitans morsitans cDNA clone Tse12H08_p1c	mRNA sequence.
ACCESSION	BX553666			
VERSION	BX553666.1	GI:33377811		
KEYWORDS	EST.			
SOURCE	Glossina morsitans morsitans			
ORGANISM	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	Lehane, M.J., Akopy, S., Gibson, W., Keshornu, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL MEDLINE PUBMED	Genome Biol. 4 (10), R63 (2003)			
COMMENT	14519198			
	Contact: Hall N			
	Pathogen Sequencing Unit			
	The Sanger Institute The Wellcome Trust Genome Campus			
	Hinxton, Cambridge, CB10 1SA, UK			
	Request for clones, please contact: Mike Lehane			
	Prof. M.J. Lehane			
	School of Biological Sciences,			
	University of Wales,			
	Bangor LL57 2UW			
	All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.			
FEATURES				
SOURCE	Location/Qualifiers			
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	/clone="Tse12H08_p1c"			
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	/clone_lib="Glossina morsitans morsitans adult infected gut"			
	/note="country: Zimbabwe; EST from adult gut infected with T.brucei"			
Query Match	0.2%;	Score 17.6;	DB 1;	Length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
OY	4459	TGACCTTTT	TTTTTTTTTTT	4482
DB	4	TAGATAGT	TTTTTTTTTTTTT	27</

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
BX553766	27 bp mRNA	BX553766	1	GI:33377899	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
FEATURES	source	1..27											
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	/tissue type="adult infected gut"												
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	/note="country: Zimbabwe; EST from adult gut infected with T.Brucei"												
Query Match	0.2%; Score 17.6; DB 1; Length 27;												
Best Local Similarity	83.3%; Pred. No. 9e+02;												
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;												
Oy	4459 TGACCTTTTTTTTTTTTTTTTTT 4482												
DB	4 TAGATAGTTTTTTTTTTTTTTTTT 27												
RESULT 962													
BX554327	27 bp mRNA	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
LOCUS	27 bp mRNA	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
DEFINITION	Glossina morsitans morsitans adult infected gut	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
ACCESSION	Glossina morsitans morsitans adult infected gut	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
VERSION	Glossina morsitans morsitans adult infected gut	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
KEYWORDS	Glossina morsitans morsitans adult infected gut	BX554327	1	GI:33378417	EST	Glossina morsitans morsitans		Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
SOURCE													



Db	4 TAGATAGTTTTTTTTTTTTTTTTTTT 27
RESULT 965	BX555155 27 bp mRNA linear EST 10-OCT-2003
LOCUS	BX555155
DEFINITION	morsitans morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse19g11_p1c, mRNA sequence.
ACCESSION	BX555155
VERSION	BX555155.1 GI:33379174
KEYWORDS	EST.
SOURCE	Glossina morsitans morsitans
ORGANISM	Glossina morsitans morsitans
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
TITLE	1 (bases 1 to 27)
JOURNAL	Lehane,M.J., Akroy,S., Gibson,W., Kephornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.P., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
MEDLINE	Genome Biol. 4 (10), R63 (2003)
PUBMED	22881942
COMMENT	14519198 Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.U.Lehane School of Biological Sciences, University of Wales, Bangor IL57 2UW All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse19g11_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with 'T.brucei'"  Query Match 0.2%; Score 17.6; DB 1; Length 27; Best Local Similarity 83.3%; Pred. No. 9e+02; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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LOCUS	BX555385
DEFINITION	morsitans morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse20b09_p1c, mRNA sequence.
ACCESSION	BX555385
VERSION	BX555385.1 GI:33379380
KEYWORDS	EST.
SOURCE	Glossina morsitans morsitans
ORGANISM	Glossina morsitans morsitans
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
TITLE	1 (bases 1 to 27)
JOURNAL	
MEDLINE	
PUBMED	
COMMENT	
FEATURES	
source	

JOURNAL AUTHORS  
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
JOURNAL MEDLINE Genome Biol. 4 (10), R63 (2003)  
PUBMED 22881942  
COMMENT 14519198  
Contact: Hall N  
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The Sanger Institute The Wellcome Trust Genome Campus  
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Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

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DB 4 TAGATAGCTTTTTTTTTTTTTTTTTT 27

RESULT 967  
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LOCUS BX555500 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21a01\_plc, mRNA sequence.  
ACCESSION BX555500  
VERSION BX555500.1 GI:33379491  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippodroscoidea; Glossinidae; Glossina.  
1 (bases 1 to 27)  
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
JOURNAL MEDLINE Genome Biol. 4 (10), R63 (2003)  
PUBMED 22881942  
COMMENT 14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
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Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

## FEATURES

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Location/Qualifiers

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTCTTTTCTTTTCTTTT 4482

Db 4 TAGATAGTTTTTTTTTTTTTTT 27

## RESULT 968

BX555567

LOCUS

BX555567 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21d12\_plc, mRNA sequence.

ACCESSION

BX555567

VERSION

BX555567.1

KEYWORDS

SOURCE

ORGANISM

EST.

Glossina morsitans morsitans

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

Location/Qualifiers

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/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse21d12\_plc"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

0.2%; Score 17.6; DB 1; Length 27;

Query Match

Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTCTTTTCTTTTCTTTT 4482

Db 4 TAGATAGTTTTTTTTTTTTTTT 27

## RESULT 969

BX555594

LOCUS

BX555594 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21f02\_plc, mRNA sequence.

DEFINITION

BX555594

VERSION

BX555594.1

KEYWORDS

SOURCE

ORGANISM

EST.

Glossina morsitans morsitans

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

Location/Qualifiers

1.27

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse21f02\_plc"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

0.2%; Score 17.6; DB 1; Length 27;

Query Match

Best Local Similarity 83.3%; Pred. No. 9e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTCTTTTCTTTTCTTTT 4482

Db 4 TAGATAGTTTTTTTTTTTTTTT 27

## RESULT 970

BX555829

LOCUS

BX555829 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse23b06\_plc, mRNA sequence.

DEFINITION

BX555829

VERSION

BX555829.1

KEYWORDS

SOURCE

Glossina morsitans morsitans

EST.

0.2%; Score 17.6; DB 1; Length 27;

Query Match

ORGANISM	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	1 (bases 1 to 27) Lehane, M.J., Aksey, S., Gibson, M., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL	Genome Biol. 4 (10), R63 (2003)			
MEDLINE	22881942			
PUBMED	14519198			
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse23506_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"			
FEATURES	source			
Query Match	0.2%;	Score 17.6;	DB 1;	Length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
Cy	4459	TGGACTTTT	TTTTTTTTTTT	4462
Db	4	TAGATAGT	TTTTTTTTTTTTT	27
RESULT 971				
LOCUS	BX555864 27 bp mRNA linear EST 10-OCT-2003			
DEFINITION	BX555864 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse23d05_p1c, mRNA sequence.			
ACCESSION	BX555864			
VERSION	BX555864.1 GI:33379834			
KEYWORDS	EST.			
ORGANISM	Glossina morsitans morsitans			
SOURCE	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	1 (bases 1 to 27) Lehane, M.J., Aksey, S., Gibson, M., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL	Genome Biol. 4 (10), R63 (2003)			
MEDLINE	22881942			
PUBMED	14519198			
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK			

```

Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
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        1. .27
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            /mol_type="mRNA"
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            /clone="Tse23d05_plc"
            /tissue_type="adult infected gut"
            /clone_1fb="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.Brucei"

Query Match          0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      4459  TCGACTTTTCTTTTCTTTTCTTTT 4482
          ||| ||||| ||||| ||||| |||||
Db      4  TAGATAGCTTTTCTTTTCTTTTCTTTT 27

RESULT 972
BX555901
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BX555901          27 bp  mRNA          linear  EST 10-OCT-2003
BX555901 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse23f02_plc, mRNA sequence.
BX555901
BX555901.1 GI:33379871
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidea; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
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            /tissue_type="adult infected gut"
            /clone_1fb="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.Brucei"

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PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
source location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/clone="Tse25c09\_pic"  
/tissue\_type="adult infected gut"  
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 9e+02; Mismatches 20; Conservative 0; Indels 4; Gaps 0;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4459 TGCACCTTTTCTTTTCTTTT 4482  
DB 4 TAGATAGTTTTTTTTTTTTTTT 27

RESULT 976 27 bp mRNA linear EST 10-OCT-2003  
BX556515  
LOCUS BX556515 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse27f09\_pic, mRNA sequence.  
ACCESSION BX556515.1 GI:33427775  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 27)

REFERENCE  
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198

COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
source location/Qualifiers  
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/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"

/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse27f09\_pic"  
/tissue\_type="adult infected gut"  
/clone\_idb="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 9e+02; Mismatches 20; Conservative 0; Indels 4; Gaps 0;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4459 TGCACCTTTTCTTTTCTTTT 4482  
DB 4 TAGATAGTTTTTTTTTTTTTTT 27

RESULT 977 27 bp mRNA linear EST 10-OCT-2003  
BX557271  
LOCUS BX557271 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse31c08\_pic, mRNA sequence.  
ACCESSION BX557271  
VERSION BX557271.1 GI:33428470  
KEYWORDS  
SOURCE  
ORGANISM

Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 27)

REFERENCE  
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198

COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
source location/Qualifiers  
1..27  
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/clone="Tse31c08\_pic"  
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 9e+02; Mismatches 20; Conservative 0; Indels 4; Gaps 0;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4459 TGCACCTTTTCTTTTCTTTT 4482  
DB 4 TAGATAGTTTTTTTTTTTTTTT 27

FEATURES	SOURCE	location/Qualifiers
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	/clone_type="adult infected gut"	
	/clone_1fb="Glossina morsitans morsitans adult infected gut"	
	/note="country: Zimbabwe; EST from adult gut infected with T.brucei"	
Query Match	0.2%;	Score 17.6; DB 1; Length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;
Matches	20; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Cy	4459	TGACCTTTTTTTTTTTTTTTT 4482
Db	4	TAGATAGTTTTTTTTTTTTTTT 27
RESULT 980	LOCUS	BX558430 27 bp mRNA linear EST 10-OCT-2003
	DEFINITION	BX558430 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse38e12_plc, mRNA sequence.
	ACCESSION	BX558430
	VERSION	BX558430.1 GI:33365138
	KEYWORDS	EST.
	SOURCE	Glossina morsitans morsitans
	ORGANISM	Glossina morsitans morsitans
	REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
	AUTHORS	1 (bases 1 to 27) Lehane, M.J., Atsoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
	TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
	JOURNAL	Genome Biol. 4 (10), R63 (2003)
	MEDLINE	22881942
	PUBMED	14519198
	COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.



Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE  
1 (bases 1 to 27)  
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL  
MEDLINE  
PUBMED  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

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source  
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/tissue\_type="adult infected gut"  
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match  
Best Local Similarity 83.3%; Pred. No. 9e+02; Length 27;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TCGACTTTTTTTTTTTTTTTT 4482  
DB 4 TAGATAGTTTTTTTTTTTTTTT 27

RESULT 984  
BX562177 27 bp mRNA linear EST 10-OCT-2003  
LOCUS BX562177 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans CDNA clone Tse5b09\_pic, mRNA sequence.  
ACCESSION BX562177 GI:33372299  
VERSION BX562177.1 GI:33372299  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 27)  
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL  
MEDLINE  
PUBMED  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane

School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
source  
1..27  
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/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match  
Best Local Similarity 83.3%; Pred. No. 9e+02; Length 27;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TCGACTTTTTTTTTTTTTTTT 4482  
DB 4 TAGATAGTTTTTTTTTTTTTTT 27

RESULT 985  
BX564083 27 bp mRNA linear EST 10-OCT-2003  
LOCUS BX564083 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans CDNA clone Tse6f02\_pic, mRNA sequence.  
ACCESSION BX564083  
VERSION BX564083.1 GI:33431280  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 27)  
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL  
MEDLINE  
PUBMED  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
source  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"



TITLE  
JOURNAL

Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

## COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source

1.27  
/organism="Trypanosoma brucei"  
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/db\_xref="taxon:5691"  
/clone="165h05"

Query Match 0.2%; Score 17.6; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5473 TTTTTCGTAAGATATTTT 5496  
|||||  
1 TTTTTCGTAAGATATTTT 24

RESULT 989  
LOCUS AW248747 19 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821119.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:282119 3',  
mRNA sequence.  
ACCESSION AW248747  
VERSION AW248747.1 GI:6591740  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE NIH-MGC <http://mgs.nci.nih.gov/>.  
JOURNAL 1 (bases 1 to 19)  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 282119.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rmail.nih.gov

Tissue Procurement: DCTD/DPB CDNA Library Preparation: ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LIML at:  
[www.bio.liml.gov/bhrp/image/image.html](http://www.bio.liml.gov/bhrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 7 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LHC5 row: P column: 16  
High quality sequence stop: 7.

FEATURES  
source

Location/Qualifiers  
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/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAC(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTCGTAAGATATTTT 4482  
|||||  
1 TTTTTCGTAAGATATTTT 19

RESULT 990  
LOCUS CF291899 19 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-108.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-108, mRNA sequence.  
ACCESSION CF291899  
VERSION CF291899.1 GI:3360932  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
TITLE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
1.19  
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/mol\_type="mRNA"  
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/issue\_type="root"  
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/lab\_host="E.coli DH10B"  
/clone\_11b="Rice root plasmid cDNA library (14ROOT)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTCGTAAGATATTTT 4482

Db 1 |||||  
1 TGTGTGTGTGTGTGT 19

## RESULT 991

CF292072

LOCUS 19 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-M03, mRNA sequence.  
CF292072  
ACCESSION CF292072.1 GI:33661105  
VERSION EST.  
KEYWORDS Oryza sativa  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTGTGTGTGT 4482  
|||  
Db 1 TGTGTGTGTGTGTGT 19

## RESULT 992

CF292144

LOCUS 19 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-N17, mRNA sequence.  
CF292144  
ACCESSION CF292144.1 GI:33661177  
VERSION EST.  
KEYWORDS Oryza sativa  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division

## FEATURES

source  
1. .19  
/organism="Oryza sativa"  
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/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
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/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."  
Query Match 0.2%; Score 17.4; DB 1; Length 19;

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source  
1. .19  
/organism="Oryza sativa"  
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/tissue\_type="root"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTGTGTGT 4482  
|||  
Db 1 TGTGTGTGTGTGT 19

## RESULT 993

CF310688/c

LOCUS 19 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.  
CF310688  
ACCESSION CF310688.1 GI:33682449  
VERSION EST.  
KEYWORDS Oryza sativa  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

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/mol\_type="mRNA"  
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/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."  
Query Match 0.2%; Score 17.4; DB 1; Length 19;





TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0248 row: K column: 13  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0248K13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114[gb|AF129072.1]) a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 4466 TTTTTTTTTTTTTTTG 4484  
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Db 19 TTTTTTTTTTTTAG 1

RESULT 997  
AZ513919 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0360E13 Mouse 10kb plasmid UGC1M library Mus musculus genomic  
DEFINITION Clone UGC1M0360E13 F, genomic survey sequence.  
ACCESSION AZ513919  
VERSION AZ513919.1 GI:10695235  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
REFERENCE  
AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

TITLE plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0360 row: B column: 13  
Seq primer: CGTTGTAAAACGACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0360E13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114[gb|AF129072.1]) a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 4464 TTTTTTTTTTTTTTTT 4482  
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Db 1 TTTTTTTTTTTT 19

RESULT 998  
AZ645841 19 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0511G04R Mouse 10kb plasmid UGC1M library Mus musculus genomic  
DEFINITION Clone UGC1M0511G04 R, genomic survey sequence.  
ACCESSION AZ645841  
VERSION AZ645841.1 GI:11775726  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
REFERENCE  
AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0511 row: G column: 04  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UUCG1M0511G04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4464 TTTTCTTTTCTTTTCTTTT 4482  
DB 1 TTTTCTTTTCTTTTCTTTT 19

RESULT 999  
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DEFINITION 1M05220N17F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
ACCESSION AZ650252  
VERSION AZ650252.1 GI:11784550  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0520 row: N column: 17  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0520N17"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4464 TTTTCTTTTCTTTTCTTTT 4482  
DB 19 TTTTCTTTTCTTTTCTTTT 1

RESULT 1000  
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DEFINITION 1M0529F08F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
ACCESSION AZ654747  
VERSION AZ654747.1 GI:11791893  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss



Oy 4464 TTTT TTTT TTTT TTTT 4482  
 Db 2 TTTT TTTT TTTT TTTT 20

## RESULT 1003

AZ307896 22 bp DNA linear GSS 29-SRP-2000  
 LOCUS 1M0010N18F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 DEFINITION clone UGCGM0010N18 F, genomic survey sequence.

ACCESSION AZ307896  
 VERSION AZ307896.1 GI:10347346  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contract: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0010 row: N column: 18  
 Seq primer: CCGTGTAAACGACGCCACGT  
 Class: plasmid ends

High quality sequence stop: 22.  
 Location/Qualifiers  
 1..22

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 /clone.lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 22;  
 Best Local Similarity 94.7%; Pred. No. 6.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4463 CTTT TTTT TTTT TTTT 4481

Db 4. CTTT CTTT TTTT TTTT 22

## RESULT 1004

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 LOCUS 2M0145J07R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 DEFINITION clone UGCGM0145J07 R, genomic survey sequence.

ACCESSION AZ845735  
 VERSION AZ845735.1 GI:13015643  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.  
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 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0145 row: J column: 07  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends

High quality sequence stop: 22.  
 Location/Qualifiers  
 1..22

## FEATURES

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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone.lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 22;  
 Best Local Similarity 94.7%; Pred. No. 6.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4470 TTTT TTTT TTTT TTTT 4488



RESULT 1007  
 AZ399663 24 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0165CT0R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0165CT0 R, genomic survey sequence.  
 ACCESSION AZ399663  
 VERSION AZ399663.1 GI:10514737  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 Rm. 308, Biomedical Polymer Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0165 row: C column: 10  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Claes: plasmid ends  
 High quality sequence sloop: 24.  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: pMD42N; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (GI:473214|9b|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 24;  
 Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4466 TTTT TTTT TTTT TTTT TTTT TTTT G 4484  
 |||||  
 Db 6 TTTTGT TTTT TTTT TTTT TTTT G 24

RESULT 1008  
 CF319499 25 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD-10-A10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa cDNA clone HD-10-A10, mRNA sequence.  
 ACCESSION CF319499  
 VERSION CF319499.1 GI:33691260  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocaridaceae; Oryzaceae; Oryza.  
 1 (bases 1 to 25)  
 Kim, J.S., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /db\_xref="taxon:4530"  
 /clone="HD-10-A10"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOPO. Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.2%; Score 17.4; DB 1; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 8.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4466 TTTT TTTT TTTT TTTT TTTT TTTT G 4484  
 |||||  
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RESULT 1009  
 AU265518 26 bp mRNA linear EST 10-MAY-2002  
 LOCUS AU265518 VS Dictyostellium discoideum cDNA clone VSP623 5', mRNA  
 DEFINITION sequence.  
 ACCESSION AU265518  
 VERSION AU265518.1 GI:20524316  
 KEYWORDS EST.  
 SOURCE Dictyostellium discoideum  
 ORGANISM Dictyostellium discoideum  
 Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
 1 (bases 1 to 26)  
 Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,  
 Takeuchi, T., Kohara, Y. and Tanaka, Y.  
 Population analysis of cDNAs from unicellular and multicellular  
 stages of Dictyostellium discoideum  
 Unpublished (2002)  
 JOURNAL Contact: Hideko Urushihara  
 COMMENT Institute of Biological Sciences  
 University of Tsukuba  
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

FEATURES  
 SOURCE  
 Tel: 81-298-53-4664  
 Fax: 81-298-53-6614  
 Email: hideko@biol.tsubuiba.ac.jp.  
 Location/Qualifiers  
 1. 26  
 /organism="Dictyostelium discoideum"  
 /mol\_type="mRNA"  
 /strain="AX4"  
 /db\_xref="taxon:44689"  
 /clone="VGS623"  
 /sex="mat A"  
 /dev\_stage="vegetative"  
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Query Match 0.2%; Score 17.4; DB 1; Length 26;  
 Best Local Similarity 94.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4463 CTTTCTTTTCTTTTCTTTT 4481  
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 8 CTCCTTTTCTTTTCTTTT 26

RESULT 1010  
 AZ818035/c 26 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M008701R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0087015 R, genomic survey sequence.

ACCESSION  
 AZ818035  
 VERSION  
 AZ818035.1 GI:12987943  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.

REFERENCE  
 AUTHORS  
 TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0087 row: 0 column: 15  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.

FEATURES  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_id="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
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 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g114732114|g5|AF129072.1), a copy-number  
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 chemically-competent E.coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 26;  
 Best Local Similarity 94.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4462 ACTTTTCTTTTCTTTTCTTTT 4480  
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 19 AATTTTCTTTTCTTTTCTTTT 1

RESULT 1011  
 AZ824574/c 28 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0099D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0099D17 F, genomic survey sequence.

ACCESSION  
 AZ824574  
 VERSION  
 AZ824574.1 GI:12994482  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.

REFERENCE  
 AUTHORS  
 TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0099 row: D column: 17  
 Seq primer: CTTGTATTAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.

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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_id="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
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 polynucleotide kinase. Adaptor oligonucleotides were



ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 77.8%; Pred. No. 1e+03;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAAAACAA 4038  
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1012  
A2836072 28 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0130K08 R, genomic survey sequence.  
ACCESSION A2836072  
VERSION A2836072.1 GI:13005980  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Plate: 0130 row: K column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers  
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FEATURES  
source  
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/mol\_type="genomic DNA"  
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/clone="UUGC2M0130K08"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 77.8%; Pred. No. 1e+03;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4013 AAATGAGAAAAAGAGAAAAACAA 4039  
Db 28 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1013  
CF328476 29 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--03-G12, mRNA sequence.  
ACCESSION CF328476  
VERSION CF328476.1 GI:33805199  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 29)

REFERENCE  
AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.-J., Kim, M.-J., Lee, T.H., Shin, Y.C.,  
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. 29

FEATURES  
source  
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/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site: 1; EcoRI; mRNA was capped  
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RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 29;  
Best Local Similarity 77.8%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAAAACAA 4038  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1014  
CF299716 30 bp mRNA linear EST 15-AUG-2003  
LOCUS CF299716/c  
DEFINITION 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

Accession CF299716 GI:3671477  
 Version CF299716.1  
 Keywords EST.  
 Source Oryza sativa  
 Organism Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 30)  
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 /organism="Oryza sativa"  
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 /cultivar="Nackdong"  
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 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAGAAACAAA 4039  
 Db 30 AAAAAAGAAACAAAAA 4

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 ACCESSION B0591372  
 VERSION B0591372.1 GI:26120955  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
 1 (bases 1 to 31)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp12-koeln.mpg.de

Insert Length: 31 Std Error: 0.00  
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 /clone\_1lb="MP12-ADIS-024-storage root"  
 /note="Vector: PCWMSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimwanzlebener Saatzzucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 17.4; DB 1; Length 31;  
 Best Local Similarity 77.8%; Pred. No. 1.2e+03;  
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAGAAACAAA 4039  
 Db 31 AAAAAAGAAACAAAAA 5

RESULT 1016  
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 LOCUS HP--08-E17.D1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--08-E17, mRNA sequence.  
 ACCESSION CF318239  
 VERSION CF318239.1 GI:33690000  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 32)  
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 /lab\_host="E.coli DH10B"  
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Db 1 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1019  
LOCUS AZ382429/c 23 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2823002.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2823002.3',  
mRNA sequence.  
ACCESSION AM245956  
KEYWORDS AM245956.1 GI:6588949  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
1 (bases 1 to 23)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2823002.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (ILNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/ILNL at:  
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality  
Scoring: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L10CM10 row: 0 column: 3  
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cloned into EcoRI/XhoI sites using the following 5'  
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insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.28; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.48; Pred. No. 7.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4485  
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1 TTTCTTTTCTTATTTTGT 22

RESULT 1020  
LOCUS AZ382429/c 23 bp DNA linear GSS 02-OCT-2000  
DEFINITION IN0139E11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0139E11 R, genomic survey sequence.

ACCESSION AZ382429  
VERSION AZ382429.1 GI:10496129  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
1 (bases 1 to 23)  
1 (bases 1 to 23)  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMP42 (g14732114|bp|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted-vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.28; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.48; Pred. No. 7.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4465 TTTT TTTT TTTT TTTT TTTT 4486  
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23 TTTT TTTT TTTT TTTT TTTT 2

RESULT 1021  
LOCUS AZ447220/c 23 bp DNA linear GSS 04-OCT-2000  
DEFINITION IN0244E15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0244E15 F, genomic survey sequence.

VERSION A2447220.1 GI:10598989  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 High quality sequence stop: 23.  
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 /note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.2; DB 1; Length 23;  
 Best Local Similarity 86.4%; Pred. No. 7.6e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTGT 4485  
 DB 23 TTTTCTTTTCTTTTCTTTTGT 2

RESULT 1022  
 A0257964/c A0257964 24 bp mRNA linear EST 25-APR-2002  
 LOCUS A0257964 3'-directed mouse CDNA library Mus musculus cDNA clone  
 DEFINITION BED0011649 3', mRNA sequence.  
 ACCESSION A0257964  
 VERSION A0257964.1 GI:20323086

KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)  
 AUTHORS Kato, K. and Matoba, R.  
 TITLE Generation of expressed sequence tags from mouse brain  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kikuya Kato  
 Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: kkatob@bs.aist-nara.ac.jp,  
 URL: http://love2.aist-nara.ac.jp/BED/index.html.  
 Location/Qualifiers  
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 /tissue\_type="Brain"  
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Query Match 0.2%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 8.3e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4471 TTTTCTTTTCTTTCTTGACA 4492  
 DB 24 TTTCTATTCTTTCTTGACA 3

RESULT 1023  
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 DEFINITION clone U001M0008601 R, genomic survey sequence.  
 ACCESSION A0207138  
 VERSION A0207138.1 GI:10345841  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 High quality sequence stop: 24.  
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.2%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5015 GAGGCTCTGGAGAGGAGC 5036  
Db 22 GAGGACACAGAGAGGAGCAGC 1

RESULT 1024  
AZS14388 24 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0361H04 F, genomic survey sequence.  
ACCESSION AZS14388  
VERSION AZS14388.1 GI:10695704  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.2%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTT 4483  
Db 2 AGTTCTCTTTTCTTTTCTTTT 23

RESULT 1025  
AZB14317/c 24 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0082C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0082C12 F, genomic survey sequence.  
ACCESSION AZB14317  
VERSION AZB14317.1 GI:12984321  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Class: plasmid ends  
High quality sequence stop: 24.  
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/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UGCGM library"  
/notes="Vector: PMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114|g0|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGAGAGAGC 3643  
DB 23 GGGGGGGGGGGAGAGGGCG 2

RESULT 1026  
LOCUS AM247153 25 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2819969.3prtime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2819969 3',  
mRNA sequence.  
ACCESSION AM247153  
KEYWORDS AM247153.1 GI:6590146  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 25)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819969.5prtime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing  
project clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.linn.gov/dbp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu/low/QualitySequence: 7 contiguous  
PHRED high quality bases following vector sequence. Very low  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LICM2 row: P column: 18  
High quality sequence stop: 7.  
Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="mRNA"

## FEATURES

source  
1..25  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db xref="taxon:9606"  
/clone="IMAGE:2819969"  
/issue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab host="PH10B (phage-resistant)"  
/clone.lib="NIH MGC 7"  
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACAG(G). Size-selected 500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17.2; DB 1; Length 25;  
Best Local Similarity 86.4%; Pred. No. 9e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4467 TTTTGTGTGTGTGTGTGT 4488  
DB 1 TTTTGTGTGTGTGTGT 22

RESULT 1027  
LOCUS AZ348233/c 25 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0084G04R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCGIM0084G04 R, genomic survey sequence.  
ACCESSION AZ348233  
VERSION AZ348233.1 GI:10427470  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
REFERENCE Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0084 row: G column: 04  
Seq primer: CACACAGAAACGCTATGACC  
Clas: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0084G04"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UGCGM library"  
/notes="Vector: PMD2nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

## FEATURES

source  
1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0084G04"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UGCGM library"  
/notes="Vector: PMD2nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.2; DB 1; Length 25;  
 Best Local Similarity 86.4%; Pred. No. 9e+02; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 3622 GGGGTGGGGTGGAGAGAGG 3643  
 Db 23 GGGGTGGGGTGGGGGGGGG 2

RESULT 1028 25 bp DNA linear GSS 31-JUL-2003  
 CC883604  
 LOCUS SALK\_095121.17.80.n Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_095121.17.80.n, genomic survey sequence.  
 ACCESSION CC883604  
 VERSION CC883604.1 GI:33359960  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (chale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 25)  
 Alonso,J.M., Leisae,T.J., Barajas,P., Chen,H., Cheuk,R., Garrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Becker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)

JOURNAL COMMENT  
 Contact: Joseph R. Becker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckers@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At2g45650. Class: TDNA tagged.

FEATURES  
 source 1..25  
 Location/Qualifiers

/organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_095121.17.80.n"  
 /clone\_1lb="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

Query Match 0.2%; Score 17.2; DB 1; Length 25;  
 Best Local Similarity 86.4%; Pred. No. 9e+02; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4485  
 Db 1 TTTGTGTGTGTGTGTGTGTGTGT 22

RESULT 1029 30 bp mRNA linear EST 29-MAY-2001  
 BG865511  
 LOCUS 602783643F1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4909811 5', mRNA sequence.  
 DEFINITION

ACCESSION BG865511  
 VERSION BG865511.1 GI:14216051  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 30)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>  
 Plate: LLM10809 row: e column: 12  
 High quality sequence stop: 30.

FEATURES

source

1..30  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4909811"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_1lb="NCI CGAP\_SG2"  
 /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1; NCI1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

Query Match 0.2%; Score 17.2; DB 1; Length 30;  
 Best Local Similarity 73.3%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAATG 4041  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAG 30

RESULT 1030 31 bp mRNA linear EST 21-FEB-2001  
 BG292912  
 LOCUS 602389549F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4501164 5', mRNA sequence.  
 DEFINITION

ACCESSION BG292912  
 VERSION BG292912.1 GI:13052227  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 31)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov

Query Match 0.2%; Score 17.2; DB 1; Length 30;  
 Best Local Similarity 73.3%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;



Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LLM10368 row: b column: 13  
 High quality sequence stop: 31.  
 Location/Qualifiers

## FEATURES

1. 31

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4501164"  
 /issue\_type="retina"  
 /lab\_host="NIH MGC 94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH MGC Library."

Query Match  
 Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAATG 4041

Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 31

## RESULT 1031

CF302459

LOCUS 32 bp mRNA linear EST 15-AUG-2003  
 7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--08-A01, mRNA sequence.

ACCESSION CF302459  
 VERSION CF302459.1 GI:33674220

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 1 (baaes 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. 32  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--08-A01"  
 /issue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match  
 Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4010 CTAAATGAGAAAAAGAGAGAAACAAATG 4039

Db 3 CAAAAAAAAAAAAAAAAAAAAAAAAA 32

## RESULT 1032

AZ579652/c

LOCUS 32 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0367C12R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0367C12 R, genomic survey sequence.

ACCESSION AZ579652  
 VERSION AZ579652.1 GI:11694081

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (baaes 1 to 32)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std. Error: 0.00

Plate: 0367 row: C column: 12

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1. 32

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0367C12"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match

0.2%; Score 17.2; DB 1; Length 32;

Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGGAAACAAATG 4041  
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAG 2

## RESULT 1033

DRIFTS/c

LOCUS DRIF7S 32 bp DNA linear GSS 27-NOV-2002  
DEFINITION Danio rerio genomic clone DKEX-1F7, genomic survey sequence.  
ACCESSION AL735323  
VERSION AL735323.1 GI:21343938  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 32)  
Humphray, S.J., Huckle, E. and Hunt, S.E.  
Direct Submission  
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
humphrey@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 1F7. 1F7 is  
part of the Daniokey BAC library created by R. Plasterk and N.V.  
Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
Location/Qualifiers  
1..32  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-1F7"  
/tissue\_type="Testis"  
/note="vector pindigobAC-536"

REFERENCE  
AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
humphrey@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 1F7. 1F7 is  
part of the Daniokey BAC library created by R. Plasterk and N.V.  
Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
Location/Qualifiers  
1..32  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-1F7"  
/tissue\_type="Testis"  
/note="vector pindigobAC-536"

FEATURES  
source

Query Match 0.2%; Score 17.2; DB 1; Length 32;  
Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4010 CTAATAATGAGAAAAAGAGGAAACAAAA 4039  
Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1034  
CF302250/c  
LOCUS 7LEAF--07-J10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION 7LEAF--07-J10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF302250  
VERSION CF302250.1 GI:33674011  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erbhatoidae; Oryzaceae; Oryza.  
1 (bases 1 to 34)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
CONTACT Contact: Nahm B.H.  
COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1..34  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultiyar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--07-J10"  
/tissue\_type="leaf"  
/dev stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="rice leaf plasmid cDNA library II (7LEAF)"  
/note="vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17.2; DB 1; Length 34;  
Best Local Similarity 73.3%; Pred. No. 1.4e+03;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4010 CTAATAATGAGAAAAAGAGGAAACAAAA 4039  
Db 34 CCAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1035  
BF338797  
LOCUS BF338797 35 bp mRNA linear EST 22-NOV-2000  
DEFINITION 602036229F1 NCI\_CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4184167  
5', mRNA sequence.  
ACCESSION BF338797  
VERSION BF338797.1 GI:11285216  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 35)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs@femail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LPM9501 row: j column: 08  
High quality sequence stop: 30.  
Location/Qualifiers  
1..35  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4184167"  
/tissue\_type="glioblastoma with EGFR amplification"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NCI\_CGAP\_Brn64"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

REFERENCE  
AUTHORS Strausberg, R., et al.  
TITLE A Gene Atlas of the Human Genome  
JOURNAL Nature  
COMMENT This is a NCI\_CGAP Library.

## FEATURES

source

Location/Qualifiers  
1..35  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4184167"  
/tissue\_type="glioblastoma with EGFR amplification"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NCI\_CGAP\_Brn64"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

Query Match 0.2%; Score 17.2; DB 1; Length 35;  
Best Local Similarity 73.3%; Pred. No. 1.5e+03;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGGAAACAAATG 4041  
Db 4 AAAAAAAAAAAAAAAAAAAAAAAAAAG 33

RESULT 1036  
 B0590687/c 17 bp mRNA linear EST 06-DEC-2002  
 LOCUS B0590687  
 DEFINITION S013717-024-018-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0590687  
 VERSION B0590687.1 GI:26120270  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 17)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 JOURNAL 22362189  
 MEDLINE 12472698  
 PUBMED  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 18 row: B column: 24  
 Seq primer: T7; GTAATACGACTCACTATAGGC.  
 Location/Qualifiers  
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 /db\_xref="GABI:189432"  
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 /clone="024-018-B24"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: PCWVSORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener SaatZucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 17; DB 1; Length 17;  
 Beet Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
 Db 17 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1037  
 B0591177 17 bp mRNA linear EST 06-DEC-2002  
 LOCUS B0591177  
 DEFINITION E0127215-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0591177  
 VERSION B0591177.1 GI:26120760  
 KEYWORDS EST.  
 SOURCE Beta vulgaris

ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 17)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 JOURNAL 22362189  
 MEDLINE 12472698  
 PUBMED  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 17 row: B column: 22  
 Seq primer: T7; GTAATACGACTCACTATAGGC.  
 Location/Qualifiers  
 1..17  
 /organism="Beta vulgaris"  
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 /db\_xref="GABI:188948"  
 /db\_xref="taxon:161934"  
 /clone="024-017-B22"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: PCWVSORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener SaatZucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 17; DB 1; Length 17;  
 Beet Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
 Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1038  
 CF290854 17 bp mRNA linear EST 14-AUG-2003  
 LOCUS CF290854  
 DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--01-A21, mRNA sequence.  
 ACCESSION CF290854  
 VERSION CF290854.1 GI:33659887  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; liliopsids; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 17)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

source

1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultiivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--01-A21"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

## RESULT 1039

CF295807

LOCUS 17 bp mRNA linear EST 14-AUG-2003  
DEFINITION 300GS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza

sativa cDNA clone 30DGS--05-O12, mRNA sequence.

ACCESSION CF295807

VERSION CF295807.1 GI:33664840

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

source

1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultiivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4468 TTTT TTTT TTTT TTTT TTTT 4484

Db 1 TTTT TTTT TTTT TTTT TTTT 17

## RESULT 1040

CF298589

LOCUS 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--02-A18, mRNA sequence.

ACCESSION CF298589

VERSION CF298589.1 GI:33670350

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

source

1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

## RESULT 1041

CF299639

LOCUS 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-L20, mRNA sequence.

ACCESSION CF299639

VERSION CF299639.1 GI:33671400

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Location/Qualifiers



REFERENCE 1 (bases 1 to 18)  
 AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.  
 TITLE EST (Koehrer, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS IngoLstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES  
 source Location/Qualifiers  
 1..18

/organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="DKFZ566L173"  
 /tissue\_type="kidney"  
 /dev\_stage="fetal"  
 /lab\_host="X1-2b1ue"  
 /clone\_lib="566 (synonym: hfk42)"  
 /note="Vector: pMPL; Site\_1: NotI; Site\_2: SalI"

Query Match 0.2%; Score 17; DB 1; Length 18;  
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4468 TTTT TTTT TTTT TTTT TTTT G 4484  
 18 TTTT TTTT TTTT TTTT TTTT G 2

RESULT 1045

CF301057 18 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION bactiva cDNA clone 7LEAF--05-M05, mRNA sequence.  
 ACCESSION CF301057  
 VERSION CF301057.1 GI:33672818  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

1..18  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 1046

CF301151 18 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION bactiva cDNA clone 7LEAF--05-005, mRNA sequence.  
 ACCESSION CF301151  
 VERSION CF301151.1 GI:33672912  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source Location/Qualifiers

1..18  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
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 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4480  
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RESULT 1047

CF327587 19 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION NACL cDNA clone NACL--02-C04, mRNA sequence.  
 ACCESSION CF327587  
 VERSION CF327587.1 GI:33803426  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division



Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
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Db 19 TTTT TTTT TTTT TTTT 3

# RESULT 1050

LOCUS A2853220 19 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M015615F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M015615 F, genomic survey sequence.

ACCESSION A2853220  
VERSION A2853220.1 GI:13041116

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Euteleostomi; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: J column: 15

Seq primer: CGTGTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

### SOURCE

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0156J15"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
|||||  
Db 19 TTTT TTTT TTTT TTTT 3

# RESULT 1051

LOCUS CP298018 20 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CP298018  
VERSION CP298018.1 GI:33669779

KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoae; Oryza.

## REFERENCE

1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

## TITLE

Unpublished (2003)

## JOURNAL

Contact: Naim B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

### SOURCE

1. .20

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--01-D19"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4468 TTTT TTTT TTTT TTTT TTTT 4484  
|||||  
Db 1 TTTT TTTT TTTT TTTT 17



RESULT 1052  
CFJ19428  
LOCUS CFJ19428 20 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD-09-020.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD-09-020, mRNA sequence.  
ACCESSION CFJ19428  
VERSION CFJ19428.1 GI:33591189  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridaceae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomic and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. 20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD-09-020"  
/tissue\_type="Callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTT 4479  
DB 1 CTTTTTTTTTTTTTTT 17

RESULT 1053  
AZ818055/c  
LOCUS AZ818055 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0087823R Mouse 10kb plasmid UGCG1M library Mus musculus genomic clone UGCG2M0087823 R, genomic survey sequence.  
ACCESSION AZ818055  
VERSION AZ818055.1 GI:12987963  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0087 row: B column: 23  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence scop: 20.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0087823"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4480  
DB 20 TTTTTTTTTTTTTTTT 4

RESULT 1054  
AL048772/c  
LOCUS AL048772 21 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZP566N143\_r1 566 (synonym: hfxd2) Homo sapiens cDNA clone  
ACCESSION AL048772  
VERSION AL048772.1 GI:4727843  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Koehrer,K., Beyer,A., Mewe,H.W., Gassenhuber,J. and Wiemann,S.  
TITLE EST (Koehrer, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.  
Location/Qualifiers

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1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ56N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfk2)"
/notes="Vector: pAMP1, Site_1: Not; Site_2: SalI"

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 21 TTTT TTTT TTTT TTTT TTTT 5

RESULT 1055
LOCUS      A2610868      21 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION clone UUGC1M0436G12 F, genomic survey sequence.
ACCESSION  A2610868
VERSION     A2610868.1 GI:11733058
KEYWORDS
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0436 row: G column: 12
            Seq primer: CGTGTAAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436G12"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to

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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1056
LOCUS      A2764492/c      21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION clone UUGC1M0560D04 R, genomic survey sequence.
ACCESSION  A2764492
VERSION     A2764492.1 GI:12879511
KEYWORDS
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0560 row: D column: 04
            Seq primer: CACACAGAAACAGCTATGAC
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0560D04"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

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ACCESSION      BK550903
VERSION        BK550903.1  GI:33374645
SOURCE         EST.
ORGANISM       Glossina morsitans morsitans
                Glossina morsitans morsitans
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Hippoosomidae; Glossinidae; Glossina.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
                Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE          Adult midgut expressed sequence tags from the tsetse fly Glossina
                morsitans and expression analysis of putative immune
                response genes
JOURNAL        Genome Biol. 4 (10), R63 (2003)
MEDLINE        22881942
PUBMED        14519198
COMMENT        Contact: Hall N
                Pathogen Sequencing Unit
                The Sanger Institute The Wellcome Trust Genome Campus
                Hinxton, Cambridge, CB10 1SA, UK
                Request for clones, please contact: Mike Lehane
                Prof. M.J.Lehane
                School of Biological Sciences,
                University of Wales,
                Bangor LL57 2UW
                All clones with suffix g1c are reverse primer reads starting at 5'
                end of the cDNA all plc reads are from
                the 3' end.
FEATURES
  source
    1..23
    /organism="Glossina morsitans morsitans"
    /mol_type="mRNA"
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    /clone_lib="Glossina morsitans morsitans adult infected
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    /note="country: Zimbabwe; EST from adult gut infected with
    T.Brucei"

Query Match      0.2%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8,1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      4464 TTTT TTTT TTTT TTTT TTTT 4480
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          1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1060
A2448207/c     24 bp DNA linear GSS 04-OCT-2000
LOCUS          1M0245E16r Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION     Clone UGCM0245E16 R, genomic survey sequence.
ACCESSION      A2448207
VERSION        A2448207.1  GI:10600777
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright D, Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
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    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-
    /clone_lib="Mouse 10kb plasmid UGCM library"
    /note="Vector: PMD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match      0.2%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8,9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      4464 TTTT TTTT TTTT TTTT TTTT 4480
          |||||
          24 TTTT TTTT TTTT TTTT TTTT 8

RESULT 1061
AU268810/c     25 bp mRNA linear EST 10-MAY-2002
LOCUS          AU268810 VS Dictyostelium discoideum cDNA clone VS1514 5', mRNA
DEFINITION     sequence.
ACCESSION      AU268810
VERSION        AU268810.1  GI:20527608
KEYWORDS       EST.
SOURCE         Dictyostelium discoideum
ORGANISM       Dictyostelium discoideum
                Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE      1 (bases 1 to 25)
AUTHORS        Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M.,
                Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE          Population analysis of cDNAs from unicellular and multicellular
                stages of Dictyostelium discoideum
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hideko Urushihara
                Institute of Biological Sciences
                University of Tsukuba
                1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                Tel: 81-298-53-4664

```

FEATURES  
source

1. 25  
/organism="Dictyostelium discoideum"  
/mol\_type="rRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSI514"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.2%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 4468 TTTTGTCTTGTCTTGA 4492  
Db 25 TTTTGTCTTGTCTTGA 1

RESULT 1062  
AM245275 25 bp mRNA linear EST 07-JUN-2000  
LOCUS 2819996.3prlme NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819996 3',  
DEFINITION mRNA sequence.  
ACCESSION AM245275  
VERSION AM245275.1 GI:6598268  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 25)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819996.5prlme  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/brrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 25 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LNC3 row: A column: 21.  
Location/Qualifiers

## FEATURES

source

1. 25  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819996"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
ScorI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 4466 TTTTGTCTTGTCTTGA 4490  
Db 1 TTTTGTCTTGTCTTGA 25

RESULT 1063  
BI094828 25 bp mRNA linear EST 14-DEC-2001  
LOCUS EST-CD34N-028 cDNA library of human CD 34+ stem/progenitor cells  
DEFINITION Homo sapiens cDNA 3', mRNA sequence.  
ACCESSION BI094828  
VERSION BI094828.1 GI:17737205  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 25)  
Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J.D. and Wang, S.M.  
The pattern of gene expression in human hematopoietic CD34+  
stem/progenitor cells  
Unpublished (2001)  
Contact: Wang SM  
Hem/Onc  
University of Chicago Medical Center  
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA  
Tel: 773-702-6788  
Fax: 773-702-3002  
Email: swangl@midway.uchicago.edu  
This EST fragment was amplified from cDNA library of human CD 34+  
stem/progenitor cells with Glgi technique (Generation of Longer  
cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.  
Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till  
the first CATG site of the target cDNA sequence.  
Seq primer: M13 Forward  
Location/Qualifiers

## FEATURES

source

1. 25  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="Bone marrow"  
/cell\_type="CD34+ stem/progenitor cells"  
/clone\_lib="cDNA library of human CD 34+ stem/progenitor  
cells"  
/note="ESTs converted from the SAGE tag sequences using  
GLGI method"

Query Match 0.2%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4472 TTTTGTCTTGTCTTGA 4496  
Db 1 TTTTGTCTTGTCTTGA 25

RESULT 1064  
CF300714 25 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-E19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION bativa cDNA clone 7LEAF--05-E19, mRNA sequence.  
ACCESSION CF300714  
VERSION CF300714.1 GI:33672475  
KEYWORDS EST.  
SOURCE Oryza sativa

```

Query Match      0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.ee+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      4468 TTTTTTTTTTTTGTCTTGAGA 4492
Db       1 TTTTTTTTTTTTGGATTGAAA 25
|||||
|||||

RESULT 1066
LOCUS      AZ659095/c
DEFINITION AZ659095 25 bp DNA linear GSS 14-DEC-2000
            IM0536E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION     AZ659095
KEYWORDS    AZ659095.1 GI:11796241
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
REFERENCE   Mus musculus
AUTHORS     Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE       1 (bases 1 to 25)
           Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausen,A. and Wright,D. Weis,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0536 row: E column: 18
            Seq primer: CGTTGTAACAGCACGCCACT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES
Source      Location/Qualifiers
             1..25
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC1M0536E18"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
             /clone_1lb="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57Bl/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adapter oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptered DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel

```

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5325 TTTTCTCTTGGCTGCTCTCC 5349  
DB 25 TCTCTCTCTCTCTCTCTCTCC 1

RESULT 1067  
LOCUS TA12F020 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 12F02, reverse sequence,  
ACCESSION AL451366  
VERSION AL451366.1 GI:11833388  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 25)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
Direct Submision  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

FEATURES  
source  
1..25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="12f02"

Query Match 0.2%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTCTCTCTCTCTCTCTCT 4480  
DB 25 TTTTCTCTCTCTCTCTCTCTCT 9

RESULT 1068  
LOCUS AU265818/c 26 bp mRNA linear EST 10-MAY-2002  
DEFINITION AU265818 VS Dictyostelium discoideum cDNA clone VSF805 5', mRNA  
sequence.

ACCESSION AU265818  
VERSION AU265818.1 GI:20524616  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
1 (bases 1 to 26)  
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,  
Takeuchi, I., Kohara, Y. and Tanaka, Y.  
Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
Unpublished (2002)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES

source  
1..26  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSF805"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.2%; Score 17; DB 1; Length 26;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4464 TTTTCTCTCTCTCTCTCTCTCT 4488  
DB 26 TTTTCTCTCTCTCTCTCTCTCT 2

RESULT 1069  
LOCUS AU268466/c 26 bp mRNA linear EST 10-MAY-2002  
DEFINITION AU268466 VS Dictyostelium discoideum cDNA clone VSI294 5', mRNA  
sequence.  
ACCESSION AU268466  
VERSION AU268466.1 GI:20527264  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
1 (bases 1 to 26)  
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,  
Takeuchi, I., Kohara, Y. and Tanaka, Y.  
Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
Unpublished (2002)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..26  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSI294"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.2%; Score 17; DB 1; Length 26;  
 Best Local Similarity 80.0%; Pred. No. 1e+03;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTT 4488  
 |||||  
 Db 26 TTTTCTTTTCTTTTCTTATT 2

RESULT 1070  
 A2828616 26 bp DNA linear GSS 20-FEB-2001  
 LOCUS  
 DEFINITION 2M0105007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0105007 R, genomic survey sequence.

ACCESSION A2828616  
 VERSION A2828616.1 GI:12998524  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weise, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0105 row: 0 column: 07  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers

## FEATURES

source

1..26  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0105007"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g1|4732114|gb|AF19072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 26;  
 Best Local Similarity 80.0%; Pred. No. 1e+03;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4450 TGGGTGCATGACCTTTTCTT 4474  
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 Db 25 TGCCTGCATGACATTTTCTTCT 1

RESULT 1071  
 AA852828 28 bp mRNA linear EST 20-JUN-2002  
 LOCUS  
 DEFINITION NHTBCae16e07f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA  
 clone NHTBCae16e07, mRNA sequence.

ACCESSION AA852828  
 VERSION AA852828.1 GI:2941421  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 28)  
 AUTHORS Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,  
 Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M.,  
 Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.  
 SCAP: The Skeletal Genome Anatomy Project  
 Unpublished (1997)  
 CONTACT: Libin Jia  
 Medical Genetics Branch  
 National Human Genome Research Institute  
 1010C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA  
 Tel: 301-402-4877  
 Fax: 301-496-7157  
 Email: libin@helix.nih.gov  
 Seq primer: M13 Forward.  
 Location/Qualifiers

## FEATURES

source

1..28  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="NHTBCae16e07"  
 /sex="Female"  
 /tissue\_type="Bone"  
 /cell\_type="Trabecular Bone Cells"  
 /lab\_host="SURE"  
 /clone\_1lb="Normal Human Trabecular Bone Cells"  
 /note="Organ: Hip; Vector: pBluescript; Site: 1. EcorI;  
 library constructed by Dr. Marian Young and Dr. Pamela  
 Gehron Robey (NIDCR)"

Query Match 0.2%; Score 17; DB 1; Length 28;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4015 ATGAGAAAAAGAGAGAAAAA 4039  
 |||||  
 Db 26 ACGAGAAAAA 2

RESULT 1072  
 DR31A15T 30 bp DNA linear GSS 22-NOV-2002  
 LOCUS  
 DEFINITION DR31A15T  
 ACCESSION AL987581  
 VERSION AL987581.1 GI:25176586  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 30)  
 HUMPHRAY, S.J., HUCKLE, E. and HUNT, S.E.



TITLE Direct Submission  
JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Camps, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 31A15. 31A15 is part of the Dadokey BAC Library created by R. Plasterk and N.V. Keygene.

Further details: [http://www.sanger.ac.uk/Projects/D\\_reio/](http://www.sanger.ac.uk/Projects/D_reio/).

FEATURES  
source Location/Qualifiers

1..30  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-31A15"  
/issue\_type="Testis"  
/note="vector pindigobAC-536"

Query Match 0.2%; Score 17; DB 1; Length 30;  
Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACA 4037  
|||||  
5 AAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 1073  
AM245279/c

LOCUS AM245279 31 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2820044.3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2820044.3', mRNA sequence.

ACCESSION AM245279  
VERSION AM245279.1 GI:6588272  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 31)  
NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT Other ESTs: 2820044.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www.bio.lnl.gov/btrp/image/image.html](http://www.bio.lnl.gov/btrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 31 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this CDNA insert was polyadenylated.

Plate: L1CM3 row: C column: 21.  
Location/Qualifiers  
1..31  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820044"  
/issue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:

FEATURES  
source

ECORI, CDNA made by oligo-dT priming. Directionally cloned into EORI/XhoI sites using the following 5' adaptor: GGACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17; DB 1; Length 31;  
Best Local Similarity 71.4%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACA 4039  
|||||  
31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1074

LOCUS BG531309 34 bp mRNA linear EST 03-APR-2001  
DEFINITION 602559543P1 NIH\_MGC\_61 Homo sapiens CDNA clone IMAGE:4697459.5', mRNA sequence.

ACCESSION BG531309  
VERSION BG531309.1 GI:13522846  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 34)  
NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC  
CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Plate: L1CM1526 row: e column: 12  
High quality sequence stop: 34.

FEATURES  
source

Location/Qualifiers  
1..34  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4697459"  
/issue\_type="embryonal carcinoma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_61"  
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgccctggcc); Site\_2: SfiI (ggcgcttggcc); Double-stranded CDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

Query Match 0.2%; Score 17; DB 1; Length 34;  
Best Local Similarity 69.7%; Pred. No. 1.5e+03;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4007 GGTCTAAATGAGAAAAAGAGAAAAACA 4039  
|||||  
2 GCGAGAAAAAAAAAAAAAAAAAAAAA 34



Query Match 0.2%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTCT 4483  
 |||||  
 Db 1 TTTTCTTTTCTTCTCT 20

## RESULT 1078

CF336815

LOCUS 20 bp mRNA linear EST 18-AUG-2003  
 DEFINITION JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence.

ACCESSION

CF336815 GI:33822012

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 20  
 Location/Qualifiers

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT--07-A04"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4468 TTTTCTTTTCTTCTCT 4487  
 |||||  
 Db 1 TTTTCTTTTCTTCTCT 20

## RESULT 1079

AZ343730

LOCUS 20 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0077E20 F, genomic survey sequence.

ACCESSION

AZ343730 GI:10422288

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS

Dunn,D., Koyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE

JOURNAL

COMMENT

CONTACT

UNIVERSITY

RM. 308,

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0077 row: E column: 20

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. 20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0077E20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g14732114[gbl]AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTCT 4483  
 |||||  
 Db 1 TTTTCTTTTCTTCTCT 20

## RESULT 1080

AZ346143/c

LOCUS 20 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0081P1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0081P1 F, genomic survey sequence.

ACCESSION

AZ346143 GI:10425380

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

AUTHORS	TITLE
Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Haml, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb

Contact: Robert B. Weiss

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
4112, USA

## Location/Qualifiers

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0081 row: P column: 11  
Seq primer: CGTTGTAAACGACGGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

## 1. .20

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UNGCIM0081P11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1kb="Mouse 10kb plasmid UNGC1 library"  
/note="Vector: PWD49N, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repeated with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD2 (g[14731119]Afr12072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

0.2%; Score 16.8; DB 1; Length 20,

Best Local Similarity 90.0%; Pred. No. 6.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

69 TTTTITTTITTTTGTCTT 4488

Db 20 TCTTTTTCCTTGTCTT 1

	20 bp	DNA	linear	GSS 13-DEC-2000
AZ633741/c	AZ633741			
LOCUS				
DEFINITION	M0489G12F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0489G12 F, genomic survey sequence.			

AZ633741.1 GI:11755931

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)

## Mus musculus

REFERENCE  
AUTHORS

Euryalota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE	Mouse whole genome scaffolding with paired end reads from 10Kt
JOURNAL	Plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center

Contact: Robert B. Weiss

Contact: Robert B. Weiss  
University of Utah  
Blommedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
Rm. 308, 84112, USA

## Location/Qualifiers

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0489 Row: G Column: 12  
 Seq primer: CGTGTGAAAACGACGGCCCGAT  
 Class: plasmid ends  
 High quality sequence scap: 20.

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U081CM0489612"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U081CM library"  
 /note="Vector: PMD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/nares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD2 (G114732114[3d]AF12972.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

0.2%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 6.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

64 TTTT TTTT TTTT TTTT 4483

Db 20 TTTGGTTTTTTTTTTTTTTT 1

AM248782	21 bp	mRNA	linear	EST 07-JAN-2000
LOCUS	AM248782			
DEFINITION	2821017_prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3', mRNA sequence.			

AW248782.1 GI:6591775

KEYWORDS	EST.
SOURCE	Homo sapiens (human)

**Homo sapiens**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 21)

AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)



Query Match 0.2%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 21 TTTT TTTT TTTT TTTT TTTT TTTT ATAG 2

RESULT 1085  
AZ468862 21 bp DNA linear GSS 04-OCT-2000  
LOCUS  
DEFINITION IM0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0282004 F, genomic survey sequence.  
ACCESSION AZ468862  
VERSION  
KEYWORDS AZ468862.1 GI:10626987  
GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0282 row: 0 column: 04  
Seq primer: CGTGTGTAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

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1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0282004"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.2%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3613 TTGGGGAATGGGGTGGGGGT 3632  
|||||  
Db 1 TTGGGGGGTGGGGTGGGGGT 20

RESULT 1086  
AZ597932 21 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION IM0412D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0412D23 F, genomic survey sequence.  
ACCESSION AZ597932  
VERSION  
KEYWORDS AZ597932.1 GI:11720122  
GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0412 row: D column: 23  
Seq primer: CGTGTGTAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES  
source  
1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0412D23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.2%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTT 4483  
 |||||  
 Db 1 TTTTCTTTTCTTTTCTTTT 20

## RESULT 1087

AZ647578

LOCUS AZ647578 21 bp DNA linear GSS 14-DEC-2000  
 DEFINITION IM0514117F Mouse 10kb plasmid UGCM library Mus musculus genomic

ACCESSION AZ647578  
 VERSION AZ647578.1 GI:11779183

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

COMMENT Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0514 row: 1 column: 17

Seq primer: CCTGTGAAACGACGCGCACT

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

source

1. 21  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCM0514117"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCM library"  
 /note="Vector: pMD42uv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTT 4483  
 |||||  
 Db 1 TTTTCTTTTCTTTTCTTTT 20

## RESULT 1088

AM246884

LOCUS AM246884 22 bp mRNA linear EST 07-JUN-2000  
 DEFINITION 2822626.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822626 3',

ACCESSION AM246884  
 VERSION AM246884.1 GI:6589877

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 22)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Other ESTs: 2822626.5prime

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: DCTP/DTF cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnl.gov/bnrg/image/image.html Base Calling / Quality

scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross\_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 20

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 22 contiguous distinct

peaks following vector sequence.

Plate: L1CM9 row: 0 column: 11

High quality sequence stop: 20.

## FEATURES

source

1. 22  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2822626"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 16.8; DB 1; Length 22;  
 Best Local Similarity 90.0%; Pred. No. 8e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTT 4482  
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Db 1 CTTTCTTTTCTTTTCTTTT 20

## RESULT 1089

AZ345485

LOCUS AZ345485 22 bp DNA linear GSS 29-SEP-2000  
 DEFINITION IM0080C02F Mouse 10kb plasmid UGCM library Mus musculus genomic





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/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/cclone="NACL--08-C13"
/risuse type="callus"
/dev stage="proliferated callus on 2n6 media for 30 days"
/lab host="E. coli DH108"
/cclone.lib="rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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QY 4467 TTTT TTTT TTTT TTTT GTC 4486  
||| ||| ||| ||| ||  
Db 1 TTTTT TTTTT TTTTT TTTACTC 20

Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel.: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```
FEATURES
  source      Location/qualifiers
              1. .24
                /organism="Oryza sativa"
                /mol_type="mrna"
                /cultivar="Nackdong"
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Query	4467	TTTTTTTTTTTTTTTGC	4486	
Db	24	TTTTTTTTTTTTTTTACTC	5	

## REFERENCE AUTHORS

**JOURNAL COMMENT** unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

**FEATURES**  
**SOURCE**

```

source
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10980"
/clones="U9GC2M0022L22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid U9GCM library"
/note="Vector: EMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```

electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4466 TTTTCTTTTCTTTTGT 4485  
Db 4 TTTTCTTTTCTTTTGT 23

RESULT 1094  
D19580/c

DEFINITION D19580 25 bp mRNA linear EST 12-DEC-1995  
MUSGS00987 Mouse 3'-directed Mus musculus domesticus cDNA clone  
mb1686 3', mRNA sequence.

ACCESSION D19580 GI:1089438  
VERSION D19580  
KEYWORDS EST.  
SOURCE Mus musculus domesticus (western European house mouse)  
ORGANISM Mus musculus domesticus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.

TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed  
cDNA sequencing  
JOURNAL Unpublished (1995)  
COMMENT Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and  
Matsubara,K.

FEATURES  
source Institute for Cellular and Molecular Biology  
Osaka University  
3-1 Yamada-oka, Suita, Osaka 565, Japan.  
Location/Qualifiers

1..25  
/organism="Mus musculus domesticus"  
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/clone\_lib="Mouse 3'-directed"

Query Match 0.2%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4466 TTTTCTTTTCTTTTGT 4485  
Db 25 TTTCTTTCTTTTCTTTGT 6

RESULT 1095  
CF282351/c  
LOCUS CF282351 28 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL-09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.

ACCESSION CF282351  
VERSION CF282351.1 GI:33659738  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretaceae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1..28  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL-09-N05"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 28;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1096  
CF321885/c

LOCUS CF321885 28 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD-13-E16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD-13-E16, mRNA sequence.

ACCESSION CF321885  
VERSION CF321885.1 GI:33693646  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretaceae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
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/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 28;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039  
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1097  
 CF330748/c 28 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF330748  
 DEFINITION sativa cDNA clone NACL--06-014, mRNA sequence.  
 ACCESSION CF330748  
 VERSION CF330748.1 GI:33809717  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 28)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 /organism="Oryza sativa"  
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 /clone="NACL--06-014"  
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 /lab\_host="E.coli DH10B"  
 /clone\_1lb="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 28;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039  
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1098  
 CF330938 28 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF330938  
 DEFINITION NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 ACCESSION CF330938  
 VERSION CF330938.1 GI:33810102  
 KEYWORDS EST.

SOURCE  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 28)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

1..28  
 /organism="Oryza sativa"  
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 /cultivar="Nackdong"  
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 /lab\_host="E.coli DH10B"  
 /clone\_1lb="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 28;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1099  
 AZ399637/c 28 bp DNA linear GSS 03-OCT-2000  
 LOCUS AZ399637  
 DEFINITION IM0165N04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0165N04 R, genomic survey sequence.  
 ACCESSION AZ399637  
 VERSION AZ399637.1 GI:10514711  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: down@genetics.utah.edu  
 Insert Length: 10000  
 Plate: 0165  
 Seq primer: CACACGAGAAACAGCTATGACC  
 Class: plasmid ends

laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [gll47311149|AR128072.1], a copy-number of inducible derivative of plasmid RL1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Qy	4012	AAATGAGAAAAAGAGAGAAAA	4035
Db	28	AAAAAAAAAAAAAAAAAAAAA	1

RESULT	1100
AZ401766	
LOCUS	AZ401766 28 bp DNA linear GSS-03-OCT-2000
DEFINITION	M00168008R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0168008 R, genomic survey sequence.

ACCESSION	72701700
VERSION	AZ401766.1
KEYWORDS	GI:10516840 GSS.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE  
1 (bases 1 to 28)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Musinae; Mus.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kbp

**JOURNAL  
COMMENT**

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

**Tel: 801 585 5606**  
**Fax: 801 585 7177**

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.000

Plate: 0168 row: 0 column: 08  
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 28.

*lab host*"E. coli strain XL10-Gold, T1-resistant, F-"/clone lib="mouse 10kb plasmid UGCG library"/note="Vector: pWMD24v; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMD2 (gi|47321414|gb|AF12072.1), a copy-number inducible derivative of plasmid T1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%	Score 16.8;	DB 1;	Length 28;
Best Local Similarity	75.0%	Pred. No. 1.2e+03;		
Matches	21;	Conservative	0;	Mismatches 7;
			Indels	0;
			Gaps	0;

QY	4012	AAAAAGAGAAATAAGAGAGAAAACAAAA	4039
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	28

RESULT 1101  
AZ471744/C

LOCUS	AZ471744	28 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	1M0286K08R Mouse 10kb plasmid U9C1M library Mus musculus genomic clone U9C1M0286K08 R, genomic survey sequence.				

VERSION AZ471744.1 GI:10629965  
KEYWORDS GSS.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL  
COMMENT**

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

**Tel: 801 585 5606**  
**Fax: 801 585 7177**

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.000

Plate: 0286 row: K column: 08  
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 28

## FEATURES

Location/Qualifiers

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/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGCM0286K08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 75.0%; Pred. No. 1.2e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAGAAACAAA 4039

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1102

AZ493138 28 bp DNA linear GSS 05-OCT-2000

LOCUS 1M0327F02R Mouse 10kb plasmid UGGCM library Mus musculus genomic

DEFINITION clone UGGCM0327F02 R, genomic survey sequence.

ACCESSION AZ493138

VERSION AZ493138.1 GI:10666359

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0327 row: F column: 02

Seq primer: CACACAGAAACGCTATAC

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

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source

source

1. .28

/organism="Mus musculus"

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGCM0327F02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 75.0%; Pred. No. 1.2e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1103

AZ653365 28 bp DNA linear GSS 14-DEC-2000

LOCUS 1M05227802F Mouse 10kb plasmid UGGCM library Mus musculus genomic

DEFINITION clone UGGCM05227802 F, genomic survey sequence.

ACCESSION AZ653365

VERSION AZ653365.1 GI:11790511

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0527 row: E column: 02

Seq primer: CGTTTAAACACGCGCACT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1. .28

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/db_xref="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g5|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 28;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1104  
AZ785035/c 28 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0028J01R Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
ACCESSION  
AZ785035  
VERSION  
AZ785035.1 GI:12921373  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0028 row: J column: 01  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 28.

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g5|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 28;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1105  
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LOCUS  
DEFINITION 2M0099109F Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
ACCESSION  
AZ824519  
VERSION  
AZ824519.1 GI:12994427  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 009 row: I column: 09  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 28.

FEATURES  
Location/Qualifiers  
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/strain="C57BL/6J"

FEATURES  
Source

1..28  
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/mol\_type="genomic DNA"

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/db xref="taxon:10090"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/narcs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [g14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

      0.2% ; Score 16.8 ; DB 1 ; Length 28 ;
Best Local Similarity 75.0% ; Pred. No. 1.2e+03 ;
Matches 21 ; Conservative 0 ; Indels 0 ; Gaps 0 ;

Query Match
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            ||||| ||||| ||||| ||||| |||||
Db         1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 28

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RESULT 1106	28 bp	DNA	linear	GSS 20-FEB-2001
LOCUS	AZ833425			
DEFINITION	280115D04R Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCG2M0115D04 R, genomic survey sequence.			
ACCESSION	AZ833425			
VERSION	AZ833425.1	GI:1300333		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 28) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genomic Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0115 row: D column: 04 Seq primer: CACACGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers 1. .28 /organism="Mus musculus" /mol_type="genomic DNA" /retain="C57BL/6J" /db_xref="taxon:10090"			
FEATURES				
Source				

RESULT 1107	
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DEFINITION	2M0177B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION	clone UUGC2M0177B08 F, genomic survey sequence.
VERSION	AZ866569
KEYWORDS	AZ866569.1 GI:13068007
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baase 1 to 28)
TITLE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Scd Error: 0.00 Plate: 0177 row: B column: 08 Seq primer: CGTTGTAAACGACGCGCCAGT Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers 1. 28 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0177B08"

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 28;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
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Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
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## RESULT 1108

TA291A010 28 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 291a01, reverse sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL486613  
 VERSION AL486613.1 GI:11853602  
 KEYWORDS GSS.

SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 28)  
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
 source location/Qualifiers

1..28  
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Query Match 0.2%; Score 16.8; DB 1; Length 28;  
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Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
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 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1109

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 LOCUS T. brucei sheared genomic DNA clone 379d11, forward sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL497637  
 VERSION AL497637.1 GI:11873359  
 KEYWORDS GSS.

SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 28)  
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
 source location/Qualifiers

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Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
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 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 1110

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 LOCUS T. brucei sheared genomic DNA clone 29a09, forward sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL453073  
 VERSION AL453073.1 GI:11854584  
 KEYWORDS GSS.

SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 28)  
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,



TITLE  
JOURNAL

Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

## COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).

Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
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DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1111  
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CF279536 29 bp mRNA linear EST 14-AUG-2003  
14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF279536  
VERSION CF279536  
KEYWORDS EST  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 29)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1.29  
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## RESULT 1112

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7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-C02, mRNA sequence.

ACCESSION CF299920  
VERSION CF299920.1 GI:33671681  
KEYWORDS EST  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 29)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

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RT-PCR."

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Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1113

CF312601 29 bp mRNA linear EST 15-AUG-2003  
ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--08-G22, mRNA sequence.

ACCESSION CF312601  
VERSION CF312601.1 GI:33684362  
KEYWORDS EST  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match  
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 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1114  
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 DEFINITION Clone UUGC1M0150D21 F, genomic survey sequence.  
 ACCESSION A2389566  
 VERSION A2389566.1 GI:10503274  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0150 row: D column: 21  
 Seq primer: CGTTGTAACACGACGCGCACT  
 Class: plasmid ends

FEATURES  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0150D21"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|g1473214|g1473214|g1473214), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
 Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1115  
 A2414283/c 29 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0186G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION Clone UUGC1M0186G12 R, genomic survey sequence.  
 ACCESSION A2414283  
 VERSION A2414283.1 GI:10538296  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0188 row: G column: 12  
 Seq primer: CACACAGAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.

FEATURES  
source

1. 29  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1117  
A2451930 29 bp DNA linear GSS 04-OCT-2000  
LOCUS A2451930.1  
DEFINITION 1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION A2451930  
VERSION A2451930.1 GI:10608203  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 29)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0251 row: E column: 05  
Seq primer: CACACAGAAACGACTATGACG  
Class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers

## source

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Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1117  
A2468402 29 bp DNA linear GSS 04-OCT-2000  
LOCUS A2468402.1  
DEFINITION 1M0281G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION A2468402  
VERSION A2468402.1 GI:10626527  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 29)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0281 row: G column: 24  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U061M0281G24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U061M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGCAAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1118  
AZ466793/c

LOCUS 29 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0315N21F Mouse 10kb plasmid U061M library Mus musculus genomic  
clone U061M0315N21 F, genomic survey sequence.

ACCESSION AZ466793  
VERSION A2486793.1 GI:10653915

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
1 (bases 1 to 29)  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: N column: 21  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 29.

FEATURES  
source

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Location/Qualifiers  
/organism="Mus musculus"

/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="U061M0315N21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U061M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGCAAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1119  
AZ661709/c

LOCUS 29 bp DNA linear GSS 14-DEC-2000  
DEFINITION 1M0540K20F Mouse 10kb plasmid U061M library Mus musculus genomic  
clone U061M0540K20 F, genomic survey sequence.

ACCESSION AZ661709  
VERSION A2661709.1 GI:11798855

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
1 (bases 1 to 29)  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0540 row: K column: 20  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 29.

FEATURES  
source

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Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"

/db\_xref="taxon:10090"  
/clone="UUGC1M0540K20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

## RESULT 1120

AZ784208

LOCUS AZ784208 29 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0026113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0026113 R, genomic survey sequence.

ACCESSION

AZ784208

VERSION

AZ784208.1 GI:12919703

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 29)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0026 row: 1 column: 13  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

FEATURES

Source

1. .29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1121

AZ806470

LOCUS AZ806470 29 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0068102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0068102 R, genomic survey sequence.

ACCESSION

AZ806470

VERSION

AZ806470.1 GI:12969849

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 29)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0068 row: 1 column: 02  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

FEATURES

Source

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

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/clone="UUGC2M0068102"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      4012 AAAATGAGAAAAAGAGGAAACAAA 4039
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1122
LOCUS      A2812242      29 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0078J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0078J15 R, genomic survey sequence.
ACCESSION  A2812242
VERSION    A2812242.1 GI:12981296
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 29)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: J column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0078J15"
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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      4012 AAAATGAGAAAAAGAGGAAACAAA 4039
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1123
LOCUS      A2868731      29 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION 2M0180L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0180L02 R, genomic survey sequence.
ACCESSION  A2868731
VERSION    A2868731.1 GI:13072338
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 29)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: L column: 02
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180L02"
/sex="Male"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGACAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1124  
TA334G090/c

LOCUS TA334G090 29 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 334g09, reverse sequence,  
genomic survey sequence.

ACCESSION AL491938  
VERSION AL491938.1 GI:11868238

KEYWORDS GSS.

SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 29)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submision

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelson@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

LOCATION/Qualifiers

1. 29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="334g09"

Query Match

0.2%; Score 16.8; DB 1; Length 29;

Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGACAAACAAA 4039  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1125  
AZ458127/c

LOCUS AZ458127 30 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0261124R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCGM0261124 R, genomic survey sequence.

ACCESSION AZ458127  
VERSION AZ458127.1 GI:10616252

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murielae; Muridae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0261 row: I column: 24

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

LOCATION/Qualifiers

1. 30  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0261124"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match  
Best Local Similarity

0.2%; Score 16.8; DB 1; Length 30;  
75.0%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
 Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1126  
 BG666435  
 LOCUS  
 DEFINITION DRRCRC02 Rat DRG Library Rattus norvegicus cDNA clone DRRCRC02 5',  
 mRNA sequence.  
 ACCESSION BG666435  
 VERSION BG666435.1 GI:13888357  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 30)  
 Xhao,H.S., Huang,Q.H., Zhang,P.X., Bao,L., Lu,Y.J., Guo,C.,  
 Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
 Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.  
 Identification of gene expression profile of dorsal root ganglion  
 in the rat peripheral axotomy model of neuropathic pain  
 Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
 22056133  
 MEDLINE  
 PUBMED 12060780  
 COMMENT Contact: Zhang Xu  
 Laboratory of Sensory System  
 Institute of Neuroscience  
 320 Yue Yang Road, Shanghai 200031, P.R.China  
 Tel: 86-21-64748700-121  
 Fax: 86-21-64713446  
 Email: xu.zhang@ion.ac.cn  
 This clone is also available at Chinese National Human Genome  
 Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
 Pudong New Area, P.R.China. Please contact with Zhang Xu  
 (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)  
 PCR primers  
 FORWARD: T3  
 BACKWARD: T7  
 Seq primer: T3  
 POLYA=No.

FEATURES  
 Source location/Qualifiers  
 1..30  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="DRRCRC02"  
 /sex="male"  
 /tissue\_type="dorsal root ganglion"  
 /dev\_stage="adult"  
 /clone\_lib="Rat DRG Library"

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
 Best Local Similarity 75.0%; Pred.No.1.4e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1127  
 CF280699/c  
 LOCUS  
 DEFINITION 14FTL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14FTL)  
 Oryza sativa cDNA clone 14FTL--07-H15, mRNA sequence.  
 ACCESSION CF280699  
 VERSION CF280699.1 GI:33658085

KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarthroideae; Oryzaceae; Oryza.  
 1 (bases 1 to 30)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

REFERENCE  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..30  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14FTL--07-H15"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Rice etiolated leaf plasmid cDNA library  
 (14FTL)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

FEATURES  
 source location/Qualifiers  
 1..30  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
 Best Local Similarity 75.0%; Pred.No.1.4e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
 Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1128  
 CF292086  
 LOCUS  
 DEFINITION 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--02-M10, mRNA sequence.  
 ACCESSION CF292086  
 VERSION CF292086.1 GI:33661119  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarthroideae; Oryzaceae; Oryza.  
 1 (bases 1 to 30)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..30  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"

FEATURES  
 source location/Qualifiers  
 1..30  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"



/db\_xref="taxon:4530"  
/clone="14ROOT--02-M10"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1129

CF299555/c 30 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--03-K01, mRNA sequence.  
ACCESSION CF299555  
VERSION CF299555.1 GI:33671316

KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 30)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..30

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="leaf"  
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/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
|||||  
30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

## RESULT 1130

CF312417/c

LOCUS ABF--08-C19.b1 ABR3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--08-C19, mRNA sequence.

ACCESSION CF312417  
VERSION CF312417.1 GI:33684178

KEYWORDS EST..gsg  
SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 30)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..30

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039  
|||||  
30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

## RESULT 1131

CF322226/c 30 bp mRNA linear EST 15-AUG-2003

LOCUS HD--13-M02.b1 OshDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--13-M02, mRNA sequence.  
DEFINITION CF322226  
ACCESSION CF322226  
VERSION CF322226.1 GI:33693987

KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 30)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1..30  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--13-M02"  
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/lab\_host="E.coli DH10B"  
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cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred.No.1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039  
DB 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1132

LOCUS CF327835 30 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza

ACCESSION CF327835

VERSION CF327835.1 GI:33803920

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 30)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
location/Qualifiers

FEATURES

source

1..30  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred.No.1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1133

LOCUS CF336555/c 30 bp mRNA linear EST 18-AUG-2003

DEFINITION JMT--06-K13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

ACCESSION CF336555

VERSION CF336555.1 GI:33821487

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 30)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
location/Qualifiers

FEATURES

source

1..30  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/clone="JMT--06-K13"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
pared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred.No.1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039  
DB 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1134

LOCUS AZ357603 30 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0099H17F Mouse 10kb plasmid tUGCIM library Mus musculus genomic

ACCESSION AZ357603

VERSION AZ357603.1 GI:10471303

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 30)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plates: 0099 row: H column: 17  
Seq primer: CCGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

## FEATURES

## SOURCE

Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0099H17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGCM library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039

Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

## RESULT 1135

AZ443322  
LOCUS AZ443322 30 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0237120R Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
clone UUCGCM0237120 R, genomic survey sequence.  
ACCESSION AZ443322  
VERSION AZ443322.1 GI:10591190  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niedermauern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

## COMMENT

University of Utah Genome Center  
University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plates: 0237 row: L column: 20  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 30.

## FEATURES

## SOURCE

Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0237L20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGCM library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039

Db 3 AAAAAAAAAAAAAAAAAAAAAAAAAA 30

## RESULT 1136

AZ455741  
LOCUS AZ455741 30 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0258D16F Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
clone UUCGCM0258D16 F, genomic survey sequence.  
ACCESSION AZ455741  
VERSION AZ455741.1 GI:10613866  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niedermauern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0258 row: D column: 16  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

#### FEATURES

source

1. .30  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0258D16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gil4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Cy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1137  
AZ481739/c 30 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0306N12F Mouse 10kb plasmid UGCC1M library Mus musculus genomic  
DEFINITION clone UGCC1M0306N12 F, genomic survey sequence.  
ACCESSION AZ481739  
VERSION AZ481739.1 GI:10642804  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 30)  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0306 row: N column: 12  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

#### FEATURES

source

1. .30  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0306N12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gil4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Cy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1138  
AZ582114/c 30 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0374J17F Mouse 10kb plasmid UGCC1M library Mus musculus genomic  
DEFINITION clone UGCC1M0374J17 F, genomic survey sequence.  
ACCESSION AZ582114  
VERSION AZ582114.1 GI:11700674  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 30)  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddun@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0374 row: J column: 17  
 Seq primer: CGTGTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence step: 30.  
 Location/Qualifiers  
 1..30

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U081M0374017"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1b="Mouse 10kb plasmid U081M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 |||||  
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1139  
 AW249485/c 31 bp mRNA linear EST 07-JAN-2000  
 LOCUS AW249485 2821429.3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2821429 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AW249485  
 VERSION AW249485.1 GI:6592478  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 31)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other ESTs: 2821429.5prime  
 Contact: Robert Strauberg, Ph.D.  
 Email: cga@bs-remail.nih.gov  
 Tissue Procurement: DCTP/DTF CDNA Library Preparation: Ling  
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/btrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross\_match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 20  
 contiguous PHRED high quality bases following vector sequence. Very  
 low Quality Sequence: Trace file contained 31 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: LCCW6 row: M column: 14  
 High quality sequence step: 20.  
 Location/Qualifiers  
 1..31

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821429"  
 /issue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="NIH MGC 7"  
 /clone\_1b="NIH MGC 7"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 |||||  
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1140  
 BX569502/c 31 bp mRNA linear EST 14-OCT-2003  
 LOCUS BX569502 Glosina morsitans morsitans adult infected gut Glosina  
 DEFINITION morsitans morsitans CDNA clone Tse9a03\_jic, mRNA sequence.  
 ACCESSION BX569502  
 VERSION BX569502.1 GI:33437420  
 KEYWORDS EST.  
 SOURCE Glosina morsitans morsitans  
 ORGANISM Glosina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 31)  
 Lehane,M.D., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glosina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 Genome Biol. 4 (10), R63 (2003)  
 22861942  
 MEDLINE 14519198  
 PUBMED  
 JOURNAL  
 COMMENT  
 Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2NW

All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from  
the 3' end.

#### FEATURES

source

Location/Qualifiers

1..31  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/db\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse9a03.plc"  
/issue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039  
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

#### RESULT 1141

LOCUS

CF278807 31 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION Oryza sativa cDNA clone 14ETL--04-N15, mRNA sequence.

VERSION CF278807.1 GI:33656193

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 31)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..31

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ETL--04-N15"

/issue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 31;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

#### RESULT 1142

LOCUS

CF300345/c

DEFINITION 7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--04-L08, mRNA sequence.

ACCESSION CF300345

VERSION CF300345.1 GI:33672106

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Eriarthroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 31)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..31

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--04-L08"

/issue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 31;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

#### RESULT 1143

LOCUS

AZ333315/c

DEFINITION 1M0062A21P Mouse 10kb plasmid UUCGIM library Mus musculus genomic

clone UUCGIM0062A21 F, genomic survey sequence.

ACCESSION AZ333315

VERSION AZ333315.1 GI:10397811

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)

Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

COMMENT

JOURNAL

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0062 row: A column: 21  
Seq primer: CGTGTGTAACGACGCGCATGCT  
Class: plasmid ends

High quality sequence stop: 31.  
Location/Qualifiers

# FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUCG1M0062A21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGGAAACAAA 4039

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

## RESULT 1144

LOCUS AZ375973 31 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0129D08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0129D08 R, genomic survey sequence.

ACCESSION AZ375973  
VERSION AZ375973.1 GI:10489673

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

## REFERENCE

AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: D column: 08  
Seq primer: CACACGAAACAGCATGACG  
Class: plasmid ends

High quality sequence stop: 31.  
Location/Qualifiers

# FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0129D08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1145

LOCUS AZ510092 31 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0354P14F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0354P14 F, genomic survey sequence.

ACCESSION AZ510092  
VERSION AZ510092.1 GI:10691408

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

## REFERENCE

AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 Row: P Column: 14  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers

FEATURES  
SOURCE

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0354P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1146  
AZ623538 31 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0461G21F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0461G21 F, genomic survey sequence.  
ACCESSION AZ623538  
VERSION AZ623538.1 GI:11745728  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weise, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0461 Row: G Column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers

FEATURES  
SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0461G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039  
|||||  
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1147  
AZ627692 31 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0469C09R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0469C09 R, genomic survey sequence.  
ACCESSION AZ627692  
VERSION AZ627692.1 GI:11749882  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weise, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

REFERENCE  
AUTHORSJOURNAL  
COMMENT



Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0469 row: C column: 09  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 31.  
 Location/Qualifiers

## FEATURES

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1.31  
 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male), was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 75.0%; Pred. No. 1.4e+03; Length 31;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1148

A2778697

LOCUS A2778697 31 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0014002F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 clone UGGCM0014002 F, genomic survey sequence.

ACCESSION A2778697  
 VERSION A2778697.1 GI:12908605

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 31)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.

Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

JOURNAL

COMMENT

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0014 row: O column: 02  
 Seq primer: CATTGTAAACAGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 31.  
 Location/Qualifiers

## FEATURES

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1.31  
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 /sex="Male"  
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 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male), was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 75.0%; Pred. No. 1.4e+03; Length 31;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1149

A2821215

LOCUS A2821215 31 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0093F21R Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 clone UGGCM0093F21 R, genomic survey sequence.

ACCESSION A2821215  
 VERSION A2821215.1 GI:12991123

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 31)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.

Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

JOURNAL

COMMENT

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0093 row: F column: 21  
Seq primer: CACACAGCAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers

FEATURES  
SOURCE

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC2M093F21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCM1 library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1150  
AZ826618 31 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0102C19F Mouse 10kb plasmid UGCM1 library Mus musculus genomic  
clone UUGC2M0102C19 F, genomic survey sequence.  
ACCESSION  
AZ826618 GI:12996442  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
MUS musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0102 row: C column: 19

Seq primer: CGTTGTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers

FEATURES  
SOURCE

1. .31  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC2M0102C19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1151  
AZ486763/c 31 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION 1M0315A11F Mouse 10kb plasmid UGCM1 library Mus musculus genomic  
clone UUGCM1M0315A11 F, genomic survey sequence.  
ACCESSION  
AZ486763 GI:10653856  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
MUS musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
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plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
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University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: A column: 11  
Seq primer: CGTTGTAAACGACGCCACT

Classes: plasmid ends  
High quality sequence scop: 31.  
Location/Qualifiers

# FEATURES

source

1. .31  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUCG1M0315A11"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAGAAACAAA 4039  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

## RESULT 1152

AM327277

LOCUS AM327277 32 bp mRNA linear EST 28-JAN-2000  
DEFINITION dg01d07.x1 NIH\_MGC\_2 Homo sapiens cDNA clone IMAGE:284628 5', mRNA sequence.

ACCESSION AM327277

VERSION AM327277.1 GI:6797772

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 32)  
NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Edge Biosystems  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Plate: LICM0028 row: G column: 13  
Seq primer: -21m3 forward primer (ABI).

Location/Qualifiers

# FEATURES

source

1. .32  
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/clone="IMAGE:284628"  
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/clone\_1ib="NIH MGC\_2"  
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1153

CF291773/c

LOCUS CF291773 32 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-F12, mRNA sequence.

ACCESSION CF291773

VERSION CF291773.1 GI:3360806

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 32)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, U.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source

1. .32  
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/db\_xref="taxon:4530"  
/clone="14ROOT--02-F12"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E. coli DH10B"  
/clone\_1ib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAGAAACAAA 4039  
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

## RESULT 1154

CF299386/c

LOCUS CF299386 32 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-G07, mRNA sequence.

ACCESSION CF299386

VERSION CF299386.1 GI:33671147

KEYWORDS EST.

```

SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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                /db_xref="taxon:4530"
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                /lab_host="E.coli DH10B"
                /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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                RT-PCR."

Query Match      0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy      4012 AAAATGAGAAAAAGAGGAAACAAA 4039
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        32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1155
LOCUS       CF309233              32 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-F14, mRNA sequence.
ACCESSION   CF309233
VERSION     CF309233.1 GI:33680994
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 32)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1..32
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                /cultiyar="Nackdong"
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FEATURES
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        /cultiyar="Nackdong"
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        /clone="ABF--03-F14"

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/tissue_type="leaf"
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy      4012 AAAATGAGAAAAAGAGGAAACAAA 4039
        |||||
        32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1156
LOCUS       CF309345/c              32 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--03-103.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-103, mRNA sequence.
ACCESSION   CF309345
VERSION     CF309345.1 GI:33681106
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 32)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1..32
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                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site_1: EcoRI; leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."

Query Match      0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy      4012 AAAATGAGAAAAAGAGGAAACAAA 4039
        |||||
        32 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1157

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LOCUS	CF313717/c	32 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	HD--01-P05.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)	Oryza sativa cDNA clone HD--01-P05	mRNA sequence.		
ACCESSION	CF313717				
VERSION	CF313717.1	GI:33685478			
KEYWORDS	EST.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eupharoidae; Oryzaceae; Oryza.				
AUTHORS	1 (bases 1 to 32)				
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.				
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs				
COMMENT	Unpublished (2003)				
CONTACT	Contact: Nahm B.H.				
GENOMICS	Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongui University				
YONGIN	Yongin, Kyonggi, Korea				
TELE	Tel: 82 31 330 6193				
FAX	Fax: 82 31 321 6355				
EMAIL	Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.				
LOCATION	Location/Qualifiers				
FEATURES	1..32				
SOURCE	/organism="Oryza sativa"				
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	/clone="HD--01-P05"				
	/tissue_type="callus"				
	/dev_stage="proliferated callus on 2M6 media for 2 weeks"				
	/lab_host="E.coli DH10B"				
	/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"				
	/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."				
Query Match	0.2%	Score 16.8;	DB 1;	Length 32;	
Best Local Similarity	75.0%	Pred. No. 1.5e+03;			
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;	
QY	4012 AAAATGAGAAAAAGAGAAAAACAAA	4039			
DB	32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5			
RESULT 1158					
LOCUS	CF321046/c	32 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	HD--12-C15.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)	Oryza sativa cDNA clone HD--12-C15	mRNA sequence.		
ACCESSION	CF321046				
VERSION	CF321046.1	GI:33692807			
KEYWORDS	EST.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eupharoidae; Oryzaceae; Oryza.				
AUTHORS	1 (bases 1 to 32)				
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.				
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs				
COMMENT	Unpublished (2003)				
CONTACT	Contact: Nahm B.H.				
GENOMICS	Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongui University				
YONGIN	Yongin, Kyonggi, Korea				
TELE	Tel: 82 31 330 6193				
FAX	Fax: 82 31 321 6355				
EMAIL	Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.				
LOCATION	Location/Qualifiers				
FEATURES	1..32				
SOURCE	/organism="Oryza sativa"				
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	/lab_host="E.coli DH10B"				
	/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"				
	/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."				
Query Match	0.2%	Score 16.8;	DB 1;	Length 32;	
Best Local Similarity	75.0%	Pred. No. 1.5e+03;			
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;	

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .32
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDACT1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="vector: pCR4-TOPO; site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match
Best Local Similarity 75.0%; Score 16.8; DB 1; Length 32;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0

OY 4012 AAAATGAGAAAAAGAGAAACAAA 4039
32 AAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1159
CEJ28471/c 32 bp mRNA linear EST 18-AUG-2001
DEFINITION NACL--03-G09_b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G09, mRNA sequence.
ACCESSION CEJ28471
VERSION CEJ28471.1 GI:33805189
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitidae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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location/Qualifiers
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: pCR4-TOPO; site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 75.0%; Score 16.8; DB 1; Length 32;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1160  
 CF331270 32 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF331270/c  
 DEFINITION NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--07-F08, mRNA sequence.  
 ACCESSION CF331270  
 VERSION CF331270.1 GI:33810751  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.,  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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 /organism="Oryza sativa"  
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 RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1161  
 AZ459536 32 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ459536/c  
 DEFINITION IM0264M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0264M16 F, genomic survey sequence.  
 ACCESSION AZ459536  
 VERSION AZ459536.1 GI:10617577  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
 COMMENT  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0264 row: M column: 16  
 Seq primer: GCTTGTAACGACGCGCACT  
 Class: plasmid ends  
 High quality sequence stop: 32.  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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 /note="Vector: PWD42nv; Purified genomic DNA from M.  
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 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1162  
 AZ470832 32 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ470832  
 DEFINITION IM0285F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0285F14 F, genomic survey sequence.  
 ACCESSION AZ470832  
 VERSION AZ470832.1 GI:10628957  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0285 row: F column: 14  
Seq primer: CCGTGTAAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 32.

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/db\_xref="taxon:10090"  
/clone="UUC1M0285F14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 0.2%; Score 16.8; DB 1; Length 32;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAGAGAGAAACAAA 4039  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

## RESULT 1163

AZ611890/c 32 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0438E02R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0438E02 R, genomic survey sequence.  
ACCESSION AZ611890  
VERSION AZ611890.1 GI:11734080  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0438 row: E column: 02  
Seq primer: CACACAGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 32.

## FEATURES

source

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/clone\_1ib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 0.2%; Score 16.8; DB 1; Length 32;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAGAGAGAAACAAA 4039  
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

## RESULT 1164

AZ778018 32 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0012020R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC2M0012020 R, genomic survey sequence.  
ACCESSION AZ778018  
VERSION AZ778018.1 GI:12907220  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddum@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0012 row: 0 column: 20  
 Seg primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 32.

## FEATURES

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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1165

DR85L21T

LOCUS DR85L21T 32 bp DNA linear GSS 22-NOV-2002  
 DEFINITION Dario rerio genomic clone DKEY-85L21, genomic survey sequence.  
 ACCESSION AL986044  
 VERSION AL986044.1 GI:25187956

KEYWORDS GSS

SOURCE Dario rerio (zebrafish)

ORGANISM Dario rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 32)  
 Humphray,S.J., Huckle,E. and Hunt,S.E.  
 Direct Submission  
 Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome  
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
 humphray@sanger.ac.uk Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Dariokey BAC library created by R. Plastek and N.V. Keygene.  
 Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

## FEATURES

source

Location/Qualifiers  
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 /clone="DKEY-85L21"  
 /issue\_type="Testis"  
 /note="vector pindigoBAC-536"

Query Match 0.2%; Score 16.8; DB 1; Length 32;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1166

CF334899/c

LOCUS CF334899/c 33 bp mRNA linear EST 18-AUG-2003  
 DEFINITION JMT--04-F19\_g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--04-F19, mRNA sequence.

ACCESSION CF334899

VERSION CF334899.1 GI:33818141

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 33)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

source

1..33  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /culturivar="Nackdong"  
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 methyltransferase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1167

BU431798/c

LOCUS BU431798/c 33 bp mRNA linear EST 09-SEP-2002  
 DEFINITION 601655890R1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3855694 3',



RNA sequence.  
 ACCESSION BU431796  
 VERSION BU431796.1 GI:22770280  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 33)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: DCTD/DRP  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 place: LHCMS70 row: c column: 23  
 High quality sequence stop: 31.  
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 /clone="IMAGE:3855694"  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: Ovary; Vector: pCMV-SPORT6; Site: 1. NotI; Site: 2. SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 Kb. Library constructed by Life Technologies."
   
  
 Query Match 0.2%; Score 16.8; DB 1; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039  
 DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 5  
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 LOCUS 14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
 DEFINITION sativa cDNA clone 14ROOT--02-B21, mRNA sequence.  
 ACCESSION CF311613  
 VERSION CF311613.1 GI:33660646  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiidae; Oryzae; Oryza.  
 1 (bases 1 to 33)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahe@gbio.com, bhnahe@bio.myongji.ac.kr.  
 FEATURES  
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 Query Match 0.2%; Score 16.8; DB 1; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039  
 DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 6  
 RESULT 1169  
 CF311229/c 33 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--06-F23, mRNA sequence.  
 ACCESSION CF311229  
 VERSION CF311229.1 GI:33682990  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiidae; Oryzae; Oryza.  
 1 (bases 1 to 33)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahe@gbio.com, bhnahe@bio.myongji.ac.kr.  
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 Query Match 0.2%; Score 16.8; DB 1; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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 DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT	1170
LOCUS	CF326967/c 33 bp mRNA linear EST 18-AUG-2003
DEFINITION	NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-E04, mRNA sequence.
ACCESSION	CF326967
VERSION	CF326967.1 GI:33802189
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungi University Yongin, Kyoeongi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnah@gpbio.com, bhnah@bio.myongji.ac.kr. Location/Qualifiers
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Query Match	0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity	75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Cy Db	4012 AAAATGAGAAAAAGAGAACAACAAA 4039
	33 AAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 1171	
LOCUS	CF328313 33 bp mRNA linear EST 18-AUG-2003
DEFINITION	NACL--03-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-C14, mRNA sequence.
ACCESSION	CF328313
VERSION	CF328313.1 GI:33804873
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungi University Yongin, Kyoeongi, Korea Tel.: 82 31 330 6193

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FEATURES
Source
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        /lab_host="E.coli DH10B"
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        /note="Vector: PCR4-TORO, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      4012 AAAATGAGAAAAAAGACAGAAACAATA 4039
||||| ||||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1172
CFJ36752          33 bp      mRNA       linear   EST 18-AUG-2003
LOCUS             JMT--06-019.G1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION        library (JMT) Oryza sativa cDNA clone JMT--06-019, mRNA sequence.
ACCESSION         CFJ36752
VERSION           CFJ36752.1 GI:33821884
KEYWORDS           EST.
SOURCE            Oryza sativa
ORGANISM          Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriharctoidae; Oryzaceae; Oryza.
REFERENCE         1 (bases 1 to 33)
AUTHORS           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE             Large-scale Sequencing Analysis of Rice ESTs
JOURNAL           Unpublished (2003)
COMMENT           Contact: Nahm B.H.
                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                  of Bioscience and Bioinformatics, Myoungji University
                  Yongin, Kyeonggi, Korea
                  Tel: 82 31 330 6193
                  Fax: 82 31 321 6355
                  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
                  Location/Qualifiers
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                        /mol_type="mRNA"
                        /cultivar="Nackdong"
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cDNA library (JMT)"
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was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis vasominate Carboxyl
methyltransferase overexpression line."

FEATURES
Source
    1..33
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="JMT--06-019"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH10B"
        /clone_idb="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
        /note="Vector: PCR4-TORO, Site 1: EcoRI, oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis vasominate Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      4012 AAAATGAGAAAAAAGACAGAAACAATA 4039
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1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

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Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 66

RESULT	1173				
CE337105/c					
LOCUS	CE337105	33 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	CE337105				
	UMT-07-G18.b1 AtUMT-overexpressing transgenic rice plasmid cDNA				
	library (UMT) Oryza sativa cDNA clone UMT-07-G18, mRNA sequence.				
ACCESSION	CE337105				
VERSION	CE337105.1	GI:33822596			
KEYWORDS	EST.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				

FEATURES	Location/Qualifiers
source	1. .33

RESULT	1174
LOCUS	AZ486795/c
DEFINITION	AZ486795 33 bp DNA linear GSS 05-OCT-2000
ACCESSION	M0315P2P Mouse 10kb plasmid tUGCIM library Mus musculus genomic clone tUGCIM0315P2 F, genomic survey sequence.
VERSION	AZ486795
KEYWORDS	AZ486795.1 GI:10653918
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33) Dunn, D., Aoyagi, A., Barber, M., Bacon, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood M., Meenen, E., Pedersen, T., Rally, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduan@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: P column: 22  
Seq primer: CGTGTGAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 33.  
Location/Qualifiers  
1..33

Query Match	0.2%	Score 16.8	DB 1	Length 33
Best Local Similarity	75.0%	Pred. No. 1.5e+03		
Matches 21	Conservative 0	Mismatches 7	Indels 0	Gaps 0

RESULT	1175
AZ627839/c	
LOCUS	
DEFINITION	33 bp DNA linear GSS 13-DEC-2000
ACCESSION	AK627839
VERSION	IM0474B02F Mouse 10kb plasmid UGCGM library Mus musculus genomic
KEYWORDS	clone UGCGM0474B02 F, genomic survey sequence.
SOURCE	AK627839
ORGANISM	GSS . GI:11750125
	Mus musculus (house mouse)
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 33)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weise,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: B column: 02  
Seq primer: GGTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 33.

## FEATURES

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1..33

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UMC1M0474B02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UMGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 33;

Best Local Similarity 75.0%; Pred. No. 1.5e+03; Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

## RESULT 1176

DR41A4T

LOCUS DR41A4T 34 bp DNA linear GSS 22-NOV-2002  
DEFINITION Danio rerio genomic clone DKEX-41A4, genomic survey sequence.

ACCESSION AJ980969

VERSION AJ980969.1 GI:25182658

KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 34)

AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphray@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 41A4. 41A4 is part of the Daniokey BAC library created by R. Plasterk and N.V.

Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
Location/Qualifiers

## FEATURES

source

1..34

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="DKEX-41A4"

/issue\_type="Testis"

/note="vector pindigobAC-536"

Query Match 0.2%; Score 16.8; DB 1; Length 34;

Best Local Similarity 75.0%; Pred. No. 1.6e+03; Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039

Db 6 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

## RESULT 1177

AU267170/c

LOCUS AU267170 23 bp mRNA linear EST 10-MAY-2002  
DEFINITION AU267170 VS Dictyostelium discoideum cDNA clone VSH269 5', mRNA sequence.

ACCESSION AU267170

VERSION AU267170.1 GI:20525968

KEYWORDS EST.

SOURCE Dictyostelium discoideum

ORGANISM Dictyostelium discoideum

REFERENCE 1 (bases 1 to 23)  
AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
Unpublished (2002)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

## JOURNAL

COMMENT

Query Match 0.2%; Score 16.6; DB 1; Length 23;

Best Local Similarity 82.6%; Pred. No. 9.4e+02; Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4465 TTTTCTTTTCTTTTCTTTTCTTTCT 4487

Db 23 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 1

## RESULT 1178

CF300172

LOCUS CF300172 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-H15.D1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-H15, mRNA sequence.

ACCESSION CF300172

VERSION CF300172.1 GI:33671933

KEYWORDS EST.

SOURCE Oryza sativa



with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 9.4e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3616 GGGATGGGCTGGGCTGGGAGA 3638  
Db 1 GTGGCTGGGCTGGGCTGGGAGA 23

## RESULT 1181

AZ469557 23 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0283A09F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M0283A09 F, genomic survey sequence.

ACCESSION AZ469557  
VERSION AZ469557.1 GI:10627682

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb

TITLE plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0283 row: A column: 09  
Seq primer: CCTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

FEATURES  
source 1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UUC1M0283A09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 9.4e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5310 TTGTGCTCTCTCTCTCTCTC 5332  
Db 1 TTGTGCTCTCTCTCTCTCTC 23

## RESULT 1182

AV740046/c 25 bp mRNA linear EST 17-OCT-2000  
LOCUS AV740046 CB Homo sapiens cDNA clone CBFAP04.5', mRNA sequence.

DEFINITION AV740046  
ACCESSION AV740046  
VERSION AV740046.1 GI:10857627

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 25)

REFERENCE Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z., Chen, S., Mac, M. and Chen, Z.  
AUTHORS Homo sapiens CB library cDNA clones  
JOURNAL Unpublished (2000)  
COMMENT Contact: Zhu Chen  
Shanghai Institute of Hematology, Rui-jin Hospital  
137 Rui-jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: mshl@ms.sh.cn  
This clone is available at Shanghai Hematology Institute in Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

TITLE  
JOURNAL  
COMMENT  
CONTACT: Zhu Chen  
SHANGHAI INSTITUTE OF HEMATOLOGY, RUI-JIN HOSPITAL  
137 RUI-JIN II ROAD, SHANGHAI 200025, P. R. CHINA  
TEL: 86-21-64740490  
FAX: 86-21-64743206  
EMAIL: mshl@ms.sh.cn  
THIS CLONE IS AVAILABLE AT SHANGHAI HEMATOLOGY INSTITUTE IN SHANGHAI.  
CHINESE NATIONAL HUMAN GENOME CENTER AT SHANGHAI  
351 GUO SHOUJING ROAD, ZHANGJIANG HI-TECH PARK, PUDONG.

FEATURES  
source 1..25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CBFAP04"  
/issue\_type="cord blood"  
/cell\_type="CD34+ hematopoietic stem/progenitor cell"  
/lab\_host="BM25.8"  
/clone\_1id="CB"  
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 0.2%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 76.0%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4467 TTTTCTTTCTTTCTTTCTTTGCTGAG 4491  
Db 25 TTTTCTTTCTTTCTTTCTTTGCTGAG 1

## RESULT 1183

BG925523/c 25 bp mRNA linear EST 06-NOV-2001  
LOCUS BG925523 HNC5-1-D5.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
DEFINITION BG925523  
ACCESSION BG925523  
VERSION BG925523.1 GI:14320046

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sachdev, G., Mol, P., Agarwal, P., Badger, A.M., Lee, D.C., Gowen, M. and Laik, M.W.  
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 URM2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay\_kumar-1@sk.com  
 Seq primer: T7.  
 FEATURES  
 source location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cblseq\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

Query Match 0.2%; Score 16.6; DB 1; Length 25;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2869 AGGAGGAGGAGGTGGGTAGG 2891  
 Db 23 AGGAGGAGGAGGAGGGAAGG 1

RESULT 1184  
 CF297950 25 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--01-C05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sative cDNA clone 7LEAF--01-C05, mRNA sequence.  
 ACCESSION CF297950  
 VERSION CF297950.1 GI:33669711  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 25)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
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 /clone\_lib="7LEAF--01-C05"  
 /cblseq\_type="leaf"  
 /dev\_stage="7 days after germination"

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sachdev, G., Mol, P., Agarwal, P., Badger, A.M., Lee, D.C., Gowen, M. and Laik, M.W.  
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 URM2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay\_kumar-1@sk.com  
 Seq primer: T7.  
 FEATURES  
 source location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cblseq\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

Query Match 0.2%; Score 16.6; DB 1; Length 25;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6467 TTTTTCCTGTTTGATATAG 6489  
 Db 1 TTTTTCCTGTTTGATATAG 23

RESULT 1185  
 AZ340193 25 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0072J03F Mouse 10kb plasmid UGCM library Mus musculus genomic  
 DEFINITION clone UGCM0072J03 F, genomic survey sequence.  
 ACCESSION AZ340193  
 VERSION AZ340193.1 GI:10415397  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0072 row: J column: 03  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence strop: 25.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_lib="UGCM0072J03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6953 GAAGGAGGGGGAATGAC 6975  
Db 24 GGAAGGAGGGGAGGAGGCGC 2

## RESULT 1186

AZ510562/c

LOCUS 25 bp DNA linear GSS 05-OCT-2000  
DEFINITION M0355F11F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0355F11 F, genomic survey sequence.

ACCESSION AZ510562  
VERSION AZ510562.1 GI:10691878

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, P., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

REFERENCE

AUTHORS

Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0355 row: F column: 11  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

FEATURES

SOURCE

1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0355F11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3615 GGGGAATGGGTGGGTGGAG 3637  
Db 23 GGGGAAGGGGGGGGGGGGGG 1

## RESULT 1187

AL048684

LOCUS 30 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZ566C043\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZ566C043, mRNA sequence.

ACCESSION AL048684  
VERSION AL048684.1 GI:4727755

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 30)  
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Koehler, et al.)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

SOURCE

1. .30  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZ566C043"  
/issue\_type="Kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_lib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.2%; Score 16.6; DB 1; Length 30;  
Best Local Similarity 82.6%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4017 GAGAAAAAGAGAAACAAA 4039  
Db 8 GAGAAAAAAGAAAAA 30

## RESULT 1188

AL048732

LOCUS 30 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZ5661053\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZ5661053, mRNA sequence.

ACCESSION AL048732  
VERSION AL048732.1 GI:4727803

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 30)  
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Koehler, et al.)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
Location/Qualifiers

FEATURES



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  1. .30
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKF2p561053"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_1ib="566 (synonym: hfxd2)"
    /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 82.6%; Score 16.6; DB 1; Length 30;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
      |||||
      8 GAGAAAAAGAGAAAAACAAA 30

RESULT 1189
R59306/c
LOCUS R59306 32 bp mRNA linear EST 24-MAY-1995
DEFINITION yhl6c10.s1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:37903 3' similar to gb:M39064 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEINS A2/B1 (HUMAN); mRNA sequence.
ACCESSION R59306 GI:830001
VERSION R59306.1 GI:830001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 32)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawking,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevashtis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: SP6
High quality sequence stop: 1.
location/Qualifiers
  1. .32
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="GDB:410444"
    /db_xref="taxon:9606"
    /clone="IMAGE:37903"
    /sex="female"
    /dev_stage="73 days post natal"
    /lab_host="DH10B (ampicillin resistant)"
    /clone_1ib="Soares infant brain INIB"
    /note="Organ: whole brain; Vector: latmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AACTGGAAGATTTCGGCCCGCAGGAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the latmid BA vector.

```

```

Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match
Best Local Similarity 71.0%; Score 16.6; DB 1; Length 32;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4009 TCTAAATGAGAAAAAGAGAAAAACAAA 4039
      |||||
      31 TCTAAGGAGAAAAAGAGAAAAACAAA 1

RESULT 1190
CF328492/c
LOCUS CF328492 34 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G22, mRNA sequence.
ACCESSION CF328492
VERSION CF328492.1 GI:33805230
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kim,J.S., Yun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnah@ggbio.com, bhnah@bio.myongji.ac.kr.
location/Qualifiers
  1. .34
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="NACL--03-G22"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 71.0%; Score 16.6; DB 1; Length 34;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4004 TTAGGCTTAAATGAGAAAAAGAGAAAAA 4034
      |||||
      31 TCATGCTTAAATGAGAAAAAGAGAAAAA 1

RESULT 1191
BM658677
LOCUS BM658677 18 bp mRNA linear EST 27-FEB-2002
DEFINITION LZV602768363.R1 CSBQFLJ37 pig adrenal Sus scrofa cDNA, mRNA
sequence.
ACCESSION BM658677
VERSION BM658677.1 GI:18958948
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

```

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Adelson, D.L. and Gill, C.A.  
 TITLE Porcine ESTs  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: David L. Adelson  
 Animal Breeding and Genetics  
 Texas A&M University  
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
 USA  
 Tel: 9798452616  
 Fax: 9798456970  
 Email: david.adelson@tamu.edu.

FEATURES  
 source Location/Qualifiers  
 1..18  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9623"  
 /clone\_id="CSEQFL37 pig adrenal"  
 /note="Organ: adrenal gland; Vector: pBluescript SK+;  
 Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert  
 (5'-NNN...NNNinsert)  
 GCGAATTCGAGCTCCACCGCGCGCGCGCGCTGAG. Sequence 3' of  
 the inserts (AAGATTGATATCAAGCTTATCGATACCGTGCAGCTGAG.  
 non-normalized library, sequenced 3' with M13R primer."

Query Match 0.2%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTCTTTCTTTCTTT 4481  
 |||||  
 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1192  
 CF300456 18 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--04-N23, mRNA sequence.  
 ACCESSION CF300456  
 VERSION CF300456.1 GI:33672217  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..18  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiVar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--04-N23"  
 /tissue\_type="leaf"  
 /dev stage="7 days after germination"  
 /lab host="E.coli DH10B"  
 /clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

FEATURES  
 source Location/Qualifiers  
 1..18  
 /organism="Oryza sativa"  
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 /tissue\_type="leaf"  
 /dev stage="7 days after germination"  
 /lab host="E.coli DH10B"  
 /clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTCTTTCTTTCTTT 4481  
 |||||  
 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1193  
 CF302409 18 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--07-N19, mRNA sequence.  
 ACCESSION CF302409  
 VERSION CF302409.1 GI:33674170  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..18  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiVar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--07-N19"  
 /tissue\_type="leaf"  
 /dev stage="7 days after germination"  
 /lab host="E.coli DH10B"  
 /clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

FEATURES  
 source Location/Qualifiers  
 1..18  
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 /cultiVar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--07-N19"  
 /tissue\_type="leaf"  
 /dev stage="7 days after germination"  
 /lab host="E.coli DH10B"  
 /clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTCTTTCTTTCTTTCTTT 4484  
 |||||  
 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1194  
 CF320046 18 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.  
 ACCESSION CF320046  
 VERSION CF320046.1 GI:33691807  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)

**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
**TITLE** Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
**JOURNAL** Large-scale Sequencing Analysis of Rice ESTs  
**COMMENT** Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**FEATURES**  
 source  
 1. 18  
 Location/Qualifiers

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDACI-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

**Query Match**  
 Best Local Similarity 94.4%; Pred. No. 6e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4464 TTTT TTTT TTTT TTTT TTTT 4481  
 |||||  
**Db** 1 TTTT TTTT TTTT TTTT AT 18

**RESULT 1195**  
**CF329137/c**  
**LOCUS** CF329137 19 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** NACL--04-P15-g1 Rice callus plasmid cDNA library (NACL) Oryza  
**ACCESSION** CF329137  
**VERSION** CF329137.1 GI:33806511  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 19)  
**REFERENCE** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
**FEATURES**  
 source  
 1. 19  
 Location/Qualifiers

/organism="Oryza sativa"  
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 /lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

**Query Match**  
 Best Local Similarity 94.4%; Pred. No. 6.8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4471 TTTT TTTT TTTT TTTT TTTT 4488  
 |||||  
**Db** 19 TTTT TTTT TTTT TTTT CT 2

**RESULT 1196**  
**CF334610**  
**LOCUS** CF334610 19 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** JMT--03-P13.b1 AcUMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.  
**ACCESSION** CF334610  
**VERSION** CF334610.1 GI:33817556  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 19)  
**REFERENCE** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
**FEATURES**  
 source  
 1. 19  
 Location/Qualifiers

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
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 /clone\_lib="AcUMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jasmonate Carboxyl  
 methyltransferase overexpression line."

**Query Match**  
 Best Local Similarity 94.4%; Pred. No. 6.8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4464 TTTT TTTT TTTT TTTT TTTT 4481  
 |||||  
**Db** 1 TTTT TTTT TTTT TTTT AT 18

**RESULT 1197**  
**AZ360314/c**  
**LOCUS** AZ360314 19 bp DNA linear GSS 02-OCT-2000  
**DEFINITION** IM0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0103G03 R, genomic survey sequence.  
**ACCESSION** AZ360314  
**VERSION** AZ360314.1 GI:10474014  
**KEYWORDS** GSS.

ORGANISM	Mus musculus
REFERENCE	Bakayocet, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhansern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: L column: 07 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. .19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGICM0560L07" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lnb="Mouse 10kb plasmid UGICM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromatically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [GII4732114 bp AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES	
SOURCE	
Query Match	0.28; Score 16.4; DB 1; Length 19;
Best Local Similarity	94.4%; Pred. No. 6.8e+02;
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
4462	ACTTTTCTTTTCTTTTCTTTT 4479
18	AAATTTTCTTTTCTTTTCTTT 1
RESULT 1199	
CF293087	
LOCUS	CF293087 21 bp mRNA linear EST 14-AUG-2003
DEFINITION	30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION	CF293087
VERSION	CF293087.1 GI:33662120
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa

ORGANISM	Mus musculus
REFERENCE	Bakayocet, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederharsen, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: L column: 07 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. .19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGICM0560L07" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lbb="Mouse 10kb plasmid UGICM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromatically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GII4732114 bp AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES	
SOURCE	
Query Match	0.28; Score 16.4; DB 1; Length 19;
Best Local Similarity	94.4%; Pred. No. 6.8e+02;
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
4462	ACTTTTCTTTTCTTTTCTTTT 4479
18	AAATTTTCTTTTCTTTTCTTTT 1
RESULT 1199	
CF293087	
LOCUS	CF293087 21 bp mRNA linear EST 14-AUG-2003
DEFINITION	30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION	CF293087
VERSION	CF293087.1 GI:33662120
KEYWORDS	EST.
ORF1	Oryza sativa
SOURCE	Oryza sativa
ORGANISM	Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1. 21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DS-02-C07"  
/issue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DS)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match  
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4469 TTTT TTTT TTTT TTTT TTTT GTC 4486  
|||||  
1 TTTT TTTT TTTT TTTT TTTT GAC 18  
Db

RESULT 1200  
LOCUS CF309614 21 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-N20.G1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.  
ACCESSION CF309614  
VERSION CF309614.1 GI:33681375  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1. 21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--03-N20"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match  
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4461 GACT TTTT TTTT TTTT TTTT TTTT 4478  
|||||  
1 GCGT TTTT TTTT TTTT TTTT 18  
Db

RESULT 1201  
LOCUS AZ316361/c 22 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0034116F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0034116 F, genomic survey sequence.  
ACCESSION AZ316361  
VERSION AZ316361.1 GI:10364110  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0034 row: 1 column: 16  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES  
source  
1. 22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0034116"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

1. 22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0034116"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative



ACCESSION CP292725 GI:33661758  
 VERSION EST.  
 KEYWORDS Oryza sativa  
 SOURCE Oryza sativa  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoae; Oryza.

REFERENCE 1 (bases 1 to 24)  
 Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

JOURNAL TITLE Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..24  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="30DS-01-K12"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DS)"  
 /note="Vector: PCR4-TOP0, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 24;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT G 4484  
 |||||  
 1 TTTT TTTT TTTT TTTT TAG 18

RESULT 1205  
 LOCUS A1000095/c 25 bp mRNA linear EST 27-AUG-1998  
 DEFINITION os61a08.g1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1609814 3' similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST; contains L1.b1 MSRI repetitive element; mRNA sequence.

ACCESSION A1000095  
 VERSION A1000095.1 GI:3190649  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 25)  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgap@nci.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 1653 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from AmerSham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1609814"  
 /sex="female, pooled"  
 /tissue\_type="breast"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CCAP Br2"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. This library is the normalized version of NCI CGAP Br1.1. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.2%; Score 16.4; DB 1; Length 25;  
 Best Local Similarity 94.4%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2417 ACACCAACATCACCACC 2434  
 |||||  
 DB 22 ACACCAACACACACACC 5

RESULT 1206  
 LOCUS A2764498/c 25 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 1M0560K04R Mouse 10kb plasmid UGCM1 library Mus musculus genomic clone UGCM10560K04 R, genomic survey sequence.

ACCESSION A2764498  
 VERSION A2764498.1 GI:12879523  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0560 row: K column: 04  
 Seq primer: CACACGAGAACACGATGACAC  
 Class: plasmid ends  
 High quality sequence stop: 25.  
 Location/Qualifiers  
 1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCM10560K04"





/clone\_11b="Mouse 10kb plasmid UUCGM library"  
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 26;  
 Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4023 AAGAGAGAAAACAAATGTTATTTT 4048  
 Db 1 AAAAAAAAAAAAAAAAAATTTTTTTT 26

RESULT 1209  
 N89936/c

LOCUS N89936 27 bp mRNA linear EST 02-APR-1996  
 DEFINITION ZB23E12.81 Soares, fetal lung NBHL19W Homo sapiens CDNA clone  
 IMAGE:302926.3 similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,  
 MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION N89936  
 VERSION N89936.1 GI:1443263  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 27)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, B., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu

FEATURES  
 source  
 1.27  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1247858"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:302926"  
 /dev\_stage="19 weeks"  
 /lab\_host="PH108 (ampicillin resistant)"  
 /clone\_11b="Soares, fetal lung NBHL19W"  
 /note="Organ: lung; Vector: pT773D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-GTTACCAATCTGAGACGGAGCGCCGCAATTTTTTTTTTT-3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT773 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Felina Bonaldi. This library was constructed  
 from the same fetus as the fetal heart library, Soares  
 fetal heart NBHL19W."

Query Match 0.2%; Score 16.4; DB 1; Length 27;  
 Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4014 AATGAGAAAAAAGAGAGAAACAAA 4039  
 Db 27 AATGCAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1210

LOCUS TA257B07P 27 bp DNA linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 257b07, forward sequence.  
 genomic survey sequence.

ACCESSION AL483278.1 GI:11849602  
 VERSION AL483278.1  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 27)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh1@sanger.ac.uk  
 COMMENT Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).

DETAILS of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.  
 Email: nelsayed@tigr.org

FEATURES  
 source  
 1.27  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="257b07"

Query Match 0.2%; Score 16.4; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAGAGAGAAAAAGAGAGAAACAAA 4038  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1211  
 LOCUS AZ812708/c 27 bp DNA linear GSS 20-FEB-2001

```

DEFINITION      2M0079M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC2M0079M06 R, genomic survey sequence.
ACCESSION       AZ358038
VERSION         AZ812708
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
REFERENCE       1 (bases 1 to 27)
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausen,A. and Wright,D., Weiss,R.
                  Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
TITLE            Unpublished (2000)
JOURNAL         Contact: Robert B. Weiss
COMMENT         University of Utah
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
                  84112, USA
                  Tel.: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plate: 0079 row: M column: 06
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                  Class: plasmid ends
                  High quality sequence stop: 27.
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                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
Query Match      0.2%; Score 16.4; DB 1; Length 27;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 1212
AZ358038      28 bp DNA linear GSS 02-OCT-2000
LOCUS        IM0100F05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION

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ACCESSION       AZ358038
VERSION         AZ358038.1 GI:10471738
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
REFERENCE       1 (bases 1 to 28)
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausen,A. and Wright,D., Weiss,R.
                  Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
TITLE            Unpublished (2000)
JOURNAL         Contact: Robert B. Weiss
COMMENT         University of Utah
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
                  84112, USA
                  Tel.: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plate: 0100 row: F column: 05
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                  Class: plasmid ends
                  High quality sequence stop: 28.
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                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
Query Match      0.2%; Score 16.4; DB 1; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 1213
R16114/c      32 bp mRNA linear EST 13-APR-1995
LOCUS        Y511F03.s2 Soares fetal liver spleen INF1S Homo sapiens cDNA clone
DEFINITION    IMAGE:66461 3' similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE

```

ACCESSION	ZETA PRECURSOR (HUMAN) ;, mRNA sequence.
VERSION	R16114
KEYWORDS	R16114.1 GI:767923
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 32)
	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holtman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Meara, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaethis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	High galley sequence starts: 1 High galley sequence stops: 1 Source: IMAGE Consortium, LUNL
Source	This clone is available royalty-free through LUNL ; contact the IMAGE Consortium (info@image.lunl.gov) for further information. Trace considered overall poor quality Seq primer: -21m13 High quality sequence stop: 1. Location/Qualifiers 1..32

Query Match	0.2%	Score 16.4	DB 1	Length 32
Best Local Similarity	69.0%	Pred. No. 1.6e+03		
Matches	20	Conservative	0	Mismatches 9; Indels 0; Gaps 0;
Qy	4011	TTAAATGAGAAAAAGAGAGAAAAACAAA	4039	
Db	30	TTAAANAAAAANAAAAANAAAAANAAAAA	2	
RESULT 1214				
A2316019/c				
LOCUS	A2316019	21 bp	DNA	linear
DEFINITION	1M0033C05R Mouse 10kb plasmid U06C1M library Mus musculus genomic			
ACCESSION	clone U06C1M0033C05 R, genomic survey sequence.			
VERSION	A2316019			
KEYWORDS	A2316019.1 GI:10363426			
SOURCE	GSS.			
ORGANISM	Mus musculus (house mouse)			
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 21)			
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hambl, C.,			

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0033 row: C column: 05  
 Seq primer: CACACAGAAACAGCATGTGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers  
 1..21

Query Match	0.2%	Score 16.2	DB 1	Length 21
Best Local Similarity	85.7%	Prod. No. 9	1e+02	
Matches 18	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY	4459	TGACATTTTTTTTTTTTTTT	4479	
Db	21	TGTGATTTTTTTTTTTTTTT	1	
RESULT 1215				
AZ345540				
LOCUS				
DEFINITION	21 bp	DNA	linear	GSS 29-SEP-2000
ACCESSION	U0080P05	Mouse 10kb plasmid	UGCGIM library	Mus musculus genomic
VERSION	AZ345540			
KEYWORDS	AZ345540.1	GI:10424777		
SOURCE	GSS.			
ORGANISM	Mus musculus	(house mouse)		
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 21)			
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,			
AUTHORS	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,			

TITLE  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
COMMENT  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
CONTACT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Biology of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: P column: 05  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

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/sex="Male"  
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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g114732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4463 CTTTCTTTCTTTCTTTCTTTT 4483  
Db 1 CTTTCTTTCTTTCTTTCTTT 21

RESULT 1216  
LOCUS A2346717 21 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0082002F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0082002 F, genomic survey sequence.  
ACCESSION A2346717  
VERSION A2346717.1 GI:10425954  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE  
Niederhausern, A. and Wright, D., Weiss, R.  
COMMENT  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
CONTACT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Biology of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: O column: 02  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g114732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4463 CTTTCTTTCTTTCTTTCTTTT 4483  
Db 1 CTTTCTTTCTTTCTTTCTTT 21

RESULT 1217  
LOCUS A2849030 21 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0150117F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC2M0150117 F, genomic survey sequence.  
ACCESSION A2849030  
VERSION A2849030.1 GI:13032696  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0150 row: 1 column: 17  
Seq primer: CCGTGTAAAACGACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
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adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**FEATURES**  
source  
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/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42n; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match** 0.2%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 3627 GGGGCTGGAGAGAGAGCTAGA 3647  
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1 GGGGAGAGAGAGAGAGAGAGA 21

**Db** 1 GGGGAGAGAGAGAGAGAGAGA 21

**RESULT 1218**  
**AZ978432** 21 bp DNA 1linear GSS 27-APR-2001  
**LOCUS** 2M0254G15R Mouse 10kb plasmid UUCG2M library Mus musculus genomic  
**DEFINITION** clone UUCG2M0254G15 R, genomic survey sequence.  
**ACCESSION** AZ978432  
**VERSION** AZ978432.1 GI:13849659  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
**REFERENCE** Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Isalam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinsley, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
**AUTHORS** Mouse whole genome scaffolding with paired end reads from 10kb  
**TITLE**

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0254 row: G column: 15  
Seq primer: CACACAGAAACGATATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUCG2M0254G15"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42n; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**FEATURES**  
source  
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/organism="Mus musculus"  
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/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42n; Purified genomic DNA from M.  
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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
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adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match** 0.2%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 3615 GGGGATGGGGTGGGGTGGGG 3635  
|||||  
1 GGGGATGGGGTGGGGTGGGG 21

**Db** 1 GGGGATGGGGTGGGGTGGGG 21

**RESULT 1219**  
**CF318882** 22 bp mRNA EST 15-AUG-2003  
**LOCUS** HD--09-C23.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
**DEFINITION** library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.  
**ACCESSION** CF318882  
**VERSION** CF318882.1 GI:33690643  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 22)  
**REFERENCE** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**AUTHORS** Large-scale Sequencing Analysis of Rice ESTs  
**TITLE** Unpublished (2003)  
**JOURNAL** Contact: Nahm B.H.  
**COMMENT**



```

Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
    source
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            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
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            /db_xref="taxon:37546"
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            T.brucei"

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Best Local Similarity 72.4%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy      4018 AGAAAAAGCAGAAAAACAATGTTATT 4046
Db      32 AAAAAAAAAAAAAAAAAAACCTTTT 4

RESULT 1224
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LOCUS
DEFINITION
  AZ759642      33 bp      DNA      linear      GSS 16-FEB-2001
  IM0552E03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0552E03 R. genomic survey sequence.
ACCESSION
  AZ759642
  AZ759642
VERSION
  AZ759642.1 GI:12866639
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
  Ismail,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausen,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0552 row: B column: 03
  Seq primer: CACACAGGAACGATATGAC
  Class: plasmid ends
  High quality sequence stop: 33.
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UOCCIM library"
/notes="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.2%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 4011 TAAATGAGAAAAGAGAAACAA 4039

DB 32 TAGAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1225  
BX558128/c

LOCUS BX558128 33 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX558128 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA Tse36g10\_p1c, mRNA sequence.

ACCESSION BX558128  
VERSION BX558128.1 GI:33429275

KEYWORDS EST.

SOURCE ORGANISM

Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 33)

Lehane, M.J., Akcey, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL 22881942  
MEDLINE 14519198  
COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane

JOURNAL 22881942  
MEDLINE 14519198  
COMMENT

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UM

All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES  
source

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Location/Qualifiers

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse36g10\_p1c"

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/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

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Query Match      0.2%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 33 GAAAAAGAGAAAACAAATGTTATT 5

RESULT 1226  
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LOCUS B0590166 16 bp mRNA linear EST 06-DEC-2002  
DEFINITION B012844-024-019-K18-T7 MP12-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-K18 3-PRIME, mRNA sequence.

ACCESSION B0590166  
VERSION B0590166.1 GI:26119749

KEYWORDS EST.

SOURCE ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H. and Radeflof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189  
MEDLINE 12472698  
COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mp12-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

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Seq primer: T7: GTAATGACATCACTATAGGCG.

FEATURES  
source

1. 16  
Location/Qualifiers

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/db\_xref="GABI:189955"

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/clone\_lib="MP12-ADIS-024-storage root"

/notes="Vector: pCMVSPORT6; Site1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfeldleber Saat-zucht AG Bielefeld, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

Spe-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BEET project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 4464 TTTT TTTT TTTT TTTT 4479  
 Db 1 TTTT TTTT TTTT TTTT 16  
 RESULT 1227  
 LOCUS B0592027  
 DEFINITION B0592027 16 bp mRNA linear EST 06-DEC-2002  
 CDNA clone 024-019-015-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0592027  
 VERSION B0592027.1 GI:26119790  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 19 row: 0 column: 15  
 Seq primer: T7; GTPATGACGACTACTATAGGAC.  
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 /note="Vector: PCWVSPO6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleimanlebenser Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 R2PD/GABI-Primary database: http://gabi.rzpd.de"

ACCESSION B0592600  
 VERSION B0592600.1 GI:26122183  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 28 row: F column: 08  
 Seq primer: SP6; ATTAGTGACACTATAGAGA.  
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 /clone="024-028-F08"  
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 /clone\_1ib="MP1Z-ADIS-024-developing root"  
 /note="Vector: PCWVSPO6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleimanlebenser Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4464 TTTT TTTT TTTT TTTT 4479  
 Db 16 TTTT TTTT TTTT TTTT 1

RESULT 1229  
 LOCUS B0592965  
 DEFINITION B0592965 16 bp mRNA linear EST 06-DEC-2002  
 CDNA clone 024-028-A01-T7 MP1Z-ADIS-024-developing root Beta vulgaris  
 ACCESSION B0592965  
 VERSION B0592965.1 GI:26122548  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,

ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research

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/mol_type="mRNA"
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/lab_host="E.coli DH10B"

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(14EUL)"  
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Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
|||||  
Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1232

CF311057

LOCUS 16 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice  
plasmid cDNA

CF311057 library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.

ACCESSION CF311057.1 GI:33682818  
VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

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then used for PCR. mRNA was prepared from ABF-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
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Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1233

CF314377

LOCUS 16 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--02-C01.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--02-C01, mRNA sequence.

ACCESSION CF314377

VERSION CF314377.1 GI:33686138

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

1..16  
/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
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Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1234

CF315789

LOCUS 16 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--04-N10.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

1..16

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/organism="Oryza sativa"
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CDNA library (HD)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4479
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      1 TTTT TTTT TTTT TTTT 16

RESULT 1235
LOCUS      CF316056      16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--05-D07.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--05-D07, mRNA sequence.
ACCESSION  CF316056
VERSION     CF316056
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
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      /mol_type="mRNA"
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      /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
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      /notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
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      reverse transcribed and then used for PCR. mRNA was
      derived from rice Histone Deacetylase overexpression
      line."

FEATURES
SOURCE

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Db 1 |||||
   1 TTTT TTTT TTTT TTTT 16

RESULT 1236
LOCUS      CF317718      16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--07-I05.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--07-I05, mRNA sequence.
ACCESSION  CF317718
VERSION     CF317718
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
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      /notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
      reverse transcribed and then used for PCR. mRNA was
      derived from rice Histone Deacetylase overexpression
      line."

FEATURES
SOURCE

Query Match      0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4479
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RESULT 1237
LOCUS      CF318894      16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HP--09-D06.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--09-D06, mRNA sequence.
ACCESSION  CF318894
VERSION     CF318894
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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      CDNA library (HD)"
      /notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
      reverse transcribed and then used for PCR. mRNA was
      derived from rice Histone Deacetylase overexpression
      line."

FEATURES
SOURCE

```

## JOURNAL COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4469 TTTT TTTT TTTT TTTT TTTT G 4484  
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1 TTTT TTTT TTTT TTTT G 16

## RESULT 1238

## LOCUS

CF320356 16 bp mRNA linear EST 15-AUG-2003  
HD--11-D14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

## ACCESSION

CF320356  
CF320356.1 GI:33692117

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Oryza sativa

## Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## Unpublished (2003)

## Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT T 4479  
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1 TTTT TTTT TTTT TTTT T 16

## RESULT 1239

## LOCUS

CF327722 16 bp mRNA linear EST 18-AUG-2003  
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-F06, mRNA sequence.

## ACCESSION

CF327722  
CF327722.1 GI:33803695

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Oryza sativa

## Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## Unpublished (2003)

## Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1. .16  
/organism="Oryza sativa"  
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/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT T 4479  
|||||  
1 TTTT TTTT TTTT TTTT T 16

## RESULT 1240

## LOCUS

CF327923 16 bp mRNA linear EST 18-AUG-2003  
NACL--02-F18.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-F18, mRNA sequence.

## ACCESSION

CF327923  
CF327923.1 GI:33804096

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Oryza sativa

## Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"

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/cultivar="Nackdong"

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/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTG 4484  
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1 TTTT TTTT TTTT TTTG 16

## RESULT 1241

CF328223 16 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--03-A10, mRNA sequence.  
ACCESSION CF328223  
VERSION CF328223.1 GI:33804692  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"

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/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTG 4484  
|||||  
1 TTTT TTTT TTTT TTTG 16

## RESULT 1242

CF333386/c 16 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.  
ACCESSION CF333386  
VERSION CF333386.1 GI:33815044  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
|||||  
1 TTTT TTTT TTTT TTTT 1

## RESULT 1243

B0590128 17 bp mRNA linear EST 06-DEC-2002  
LOCUS B012843-024-019-E19-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
DEFINITION cDNA clone 024-019-E19 3-PRIME, mRNA sequence.  
ACCESSION B0590128  
VERSION B0590128.1 GI:26119711

KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
AUTHORS 1 (bases 1 to 17)  
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnrich, H.  
and Radclouf, U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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Kleinmanleberer Saatgut AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-17; Note:  
Sequencing granted in the context of the GABI-Best  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 17;  
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QY 4464 TTTT TTTT TTTT TTTT TTTT 4479  
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RESULT 1244  
CF294668 17 bp mRNA linear EST 14-AUG-2003  
LOCUS 30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
DEFINITION sativa cDNA clone 30DGS--04-E17, mRNA sequence.  
ACCESSION CF294668  
VERSION CF294668.1 GI:33663701  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
AUTHORS Large-scale Sequencing Analysis of Rice ESTs  
TITLE

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479  
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1 TTTT TTTT TTTT TTTT 16

RESULT 1245  
CF295988 17 bp mRNA linear EST 14-AUG-2003  
LOCUS 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
DEFINITION sativa cDNA clone 30DGS--06-C17, mRNA sequence.  
ACCESSION CF295988  
VERSION CF295988.1 GI:33665021  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
AUTHORS Large-scale Sequencing Analysis of Rice ESTs  
TITLE Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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/lab\_host="E.coli DH10B"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
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Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1246

CF297251

LOCUS CF297251 17 bp mRNA linear EST 14-AUG-2003  
DEFINITION 300GS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

CF297251

VERSION sativa cDNA clone 30DGS--07-P12, mRNA sequence.

CF297251.1 GI:33666284

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

REFERENCE Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="30DGS--07-P12"

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/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT 4484

|||||

Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1247

CF298341

LOCUS CF298341 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

CF298341

VERSION sativa cDNA clone 7LEAF--01-K24, mRNA sequence.

CF298341.1 GI:33670102

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

REFERENCE Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
CONTACT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--01-K24"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT 4484

|||||

Db 1 TTTT TTTT TTTT TTTT 16

## RESULT 1248

CF302447

LOCUS CF302447 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

CF302447

VERSION sativa cDNA clone 7LEAF--07-P11, mRNA sequence.

CF302447.1 GI:33674208

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

REFERENCE Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--07-P11"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."



Query Match 0.2%; Score 16; DB 1; Length 17;  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
 |||||  
 1 TTTT TTTT TTTT TTTT 16

Db

## RESULT 1249

CF313013  
 DEFINITION CF313013 17 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.  
 ACCESSION CF313013  
 VERSION CF313013.1 GI:33684774  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 17)  
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 TITLE JOURNAL  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.2%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
 |||||  
 1 TTTT TTTT TTTT TTTT 16

Db

RESULT 1250  
 CF336950  
 LOCUS CF336950 17 bp mRNA linear EST 18-AUG-2003  
 DEFINITION JMT--07-D04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.  
 ACCESSION CF336950  
 VERSION CF336950.1 GI:33822280  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE JOURNAL  
 COMMENT Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="AcJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jasmonate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4479  
 |||||  
 1 TTTT TTTT TTTT TTTT 16

Db

RESULT 1251  
 CF300236  
 LOCUS CF300236 19 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--04-124.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--04-124, mRNA sequence.  
 ACCESSION CF300236  
 VERSION CF300236.1 GI:33671997  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 19)  
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE JOURNAL  
 COMMENT Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
 source  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--04-124"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"

/lab host="E.coli DH10B"  
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 1 TTTT TTTT TTTT TTTT G 16

## RESULT 1252

CF309636

LOCUS CF309636 19 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-008.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--03-008, mRNA sequence.

ACCESSION

CF309636

VERSION

CF309636.1 GI:33681397

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.

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Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .19

Location/Qualifiers

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--03-008"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 1 TTTT TTTT TTTT TTTT G 16

## RESULT 1253

CF311668

LOCUS

CF311668/c

DEFINITION

ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.

ACCESSION

CF311668

VERSION

CF311668

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.

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FEATURES

source

VERSION CF311668.1 GI:33683429

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .19

Location/Qualifiers

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--07-A05"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Oy 4464 TTTT TTTT TTTT TTTT TTTT T 4479  
|||||  
Db 16 TTTT TTTT TTTT TTTT T 1

## RESULT 1254

CF319596

LOCUS

HD--10-C14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.

ACCESSION

CF319596

VERSION

CF319596.1 GI:33691357

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

CONTACT: Nahm B.H.

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Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .19

Location/Qualifiers

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--07-A05"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Oy 4464 TTTT TTTT TTTT TTTT TTTT T 4479  
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Db 16 TTTT TTTT TTTT TTTT T 1

/organism="Oryza sativa"  
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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT G 16

RESULT 1255  
CF325356 19 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT1--03-A08.g1 A6JMT-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA  
sequence.  
ACCESSION CF325356  
VERSION CF325356.1 GI:33798994  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
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/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="A6JMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis thaliana Carboxyl  
methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT G 16

RESULT 1256  
CF299570 20 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--03-K09, mRNA sequence.  
ACCESSION CF299570  
VERSION CF299570.1 GI:33671331  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
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/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT T 4479  
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Db 1 TTTT TTTT TTTT TTTT TTTT T 16

RESULT 1257  
CF330490 20 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--06-D16, mRNA sequence.  
ACCESSION CF330490  
VERSION CF330490.1 GI:33809214  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

1..20

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL-06-D16"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2M6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484

Db 1 TTTT TTTT TTTT TTTT TTTT G 16

RESULT 1258

CF282313/c

LOCUS

DEFINITION 21 bp mRNA linear EST 14-AUG-2003

Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.

ACCESSION

CF282313

CF282313.1 GI:33659700

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretioideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

JOURNAL

TITLE

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

1..21

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ETL--09-M08"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484

Db 21 TTTT TTTT TTTT TTTT TTTT G 6

RESULT 1259

AZ341108/c

LOCUS

DEFINITION 21 bp DNA linear GSS 29-SEP-2000

clone U8GCM0073014 F, genomic survey sequence.

ACCESSION

AZ341108

AZ341108.1 GI:10417030

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: 0 column: 14

Seq primer: CGTTGTAAACGACGCGCAGCT

Class: plasmid ends

High quality sequence stop: 21.

location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U8GCM0073014"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1lb="Mouse 10kb plasmid U8GCM library"

/notes="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gil4732114|bp|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTT 4478-  
Db 16 CTTTCTTTTCTTTT 1

RESULT 1260  
AZ963501 21 bp DNA linear GSS 27-APR-2001  
LOCUS 2M032M07R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION Clone UGCGM0232M07 R, genomic survey sequence.  
ACCESSION AZ963501  
VERSION AZ963501.1 GI:13834728  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0232 row: M column: 07  
Seq primer: CACACAGAAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M032M07"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTTCTTTTCTTTG 4484  
Db 1 TTTTCTTTTCTTTG 16

RESULT 1261  
AZ317017 22 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0035P09F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION Clone UGCGM0035P09 F, genomic survey sequence.  
ACCESSION AZ317017  
VERSION AZ317017.1 GI:10365400  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: P column: 09  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0035P09"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 CTTTTTTTTTTTTT 22

## RESULT 1262

AM335179 23 bp mRNA linear EST 31-JAN-2000  
 LOCUS S44B AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
 ACCESSION AM335179  
 VERSION AM335179.1 GI:6831798  
 KEYWORDS EST.  
 SOURCE Pneumocystis carinii  
 ORGANISM Pneumocystis carinii  
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
 Pneumocystidaceae; Pneumocystis.

## REFERENCE

AUTHORS Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
 Edman,J.C., Kovacs,J. and Cushman,M.  
 TITLE Expressed sequence tags from Pneumocystis carinii  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY  
 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staben@pop.uky.edu.  
 Location/Qualifiers

## FEATURES

source

1..23  
 /organism="Pneumocystis carinii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4754"  
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 /clone\_lib="AGS-1"  
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
 P. carinii organisms (3x10e9) from a single rat (99-1-6,  
 sacrificed on 3/17/99) at Cincinnati VA facilities.  
 Triol extracted RNA. Oligo dt priming, standard  
 conditions described by vendor, Stratagene. Further  
 details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.2%; Score 16; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4479  
 Db 1 TTTTTTTTTTTTTT 16

## RESULT 1263

CF334146 23 bp mRNA linear EST 18-AUG-2003  
 LOCUS JMT--03-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 DEFINITION JMT--03-F05.g1 Oryza sativa cDNA JMT--03-F05, mRNA sequence.  
 ACCESSION CF334146  
 VERSION CF334146.1 GI:33816628  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

FEATURES  
 source  
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 /organism="Oryza sativa"  
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 /clone="JMT--03-F05"  
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 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis jasmonate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4479  
 Db 1 TTTTTTTTTTTTTT 16

## RESULT 1264

AZ330773/c 23 bp DNA linear GSS 29-SEP-2000  
 LOCUS AZ330773  
 DEFINITION IM005600F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
 clone UUGCIM005600 F, genomic survey sequence.  
 ACCESSION AZ330773  
 VERSION AZ330773.1 GI:10392809  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murineae; Mus.

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D. Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 Plate: 0056 row: O column: 08  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers

## FEATURES

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCIM0056008"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCIM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred.No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4469 TTTTGTGTTTGTG 4484  
|||||  
Db 23 TTTTGTGTTTGTG 8

RESULT 1265  
A0257474/C

LOCUS A0257474 24 bp mRNA linear EST 25-APR-2002  
DEFINITION A0257474 3'-directed mouse cDNA library Mus musculus cDNA clone

ACCESSION BED0010682 3', mRNA sequence.  
A0257474

VERSION A0257474.1 GI:20322129  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 24)  
Kato, K. and Matoba, R.  
Generation of expressed sequence tags from mouse brain  
Unpublished (2002)

CONTACT: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takeyama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5589  
Email: kkatods@ist-nara.ac.jp,  
URL: <http://love2.ist-nara.ac.jp/BED/index.html>.

FEATURES  
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1..24  
Location/Qualifiers

/organism="Mus musculus"  
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/clone="BED0010682"  
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/clone\_id="3'-directed mouse cDNA library"

Query Match 0.2%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred.No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3271 TTTGTTAAGAGAAAATGAAC 3294  
|||||  
Db 24 TTTGTTAAGAGAAAATGAATC 1

RESULT 1266  
CF327904 CF327904 24 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-J06, mRNA sequence.  
ACCESSION CF327904  
VERSION CF327904.1 GI:33804058  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriacridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: [bhnam@gsbio.com](mailto:bhnam@gsbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

FEATURES  
source  
1..24  
Location/Qualifiers

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--02-J06"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_id="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred.No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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|||||  
Db 1 TTTTTCGTTTAAATATGC 24

RESULT 1267  
A2308225

LOCUS A2308225 24 bp DNA linear GSS 29-SEP-2000  
DEFINITION A2308225 Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM001B06 F, genomic survey sequence.

ACCESSION A2308225  
VERSION A2308225.1 GI:10348004  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

JOURNAL  
COMMENT

Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0011 row: E column: 06  
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/clone="MUSGCM0011B06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCGIM library"  
/note="Vector: PMD424; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114[GB|AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

```

Query Match Similarity 0.28; Score 16; DB 1; length 24;
Best Local Similarity 79.28; Pred No. 1.2e-03;
Matches 19; Conservative 0; Mismatches 5; Indels 0;
Gaps 0;

QY 4462 ACTTTTCTTTTTTTTTTTTTTGT 4485
  |||||
Db 1 AGTTTTTGGTTTGTGTTTTT 24

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RESULT	1268
A234908	
LOCUS	A234908 24 bp DNA linear GSS 29-SEP-2000
DEFINITION	1M0085013R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0085013 R, genomic survey sequence.

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Insert length: 10000    Std Error: 0.000
Place: 0085    row: 0    column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UTGCTM0085013"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UTGCTM library"  
/note="Vector: PWDm2a1; Purified genomic DNA from M.  
musculus C57BL/6J (male); was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114|sb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query	March	0.2%	Score	16	DB	1	Length	24	
Best	Local	Similarity	79.2%	Pred.	No.	1.2e+03			
Matches	19	Conservative	0	Mismatches	5	Indels	0	Gaps	0
OY	4462	ACTTTTCTTTTTTTTTTTTTTTTGT	4485						
DB	1	AGTGTGTCGTTTTTTTTTTTTTT	24						

RESULT	1269
AZ805931	
LOCUS	24 bp DNA linear
DEFINITION	2M0067P02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0067P02 R, genomic survey sequence.





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ACCESSION      AT492371
VERSION        AL492371.1  GI:11867375
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
                Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
                Trypanosoma.
REFERENCE      1 (bases 1 to 26)
AUTHORS       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.B., Rajandream,M.A. and Barrell,B.G.
TITLE         Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus,
                Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),
                Rockville, MD. Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                to give a tight size distribution (
                4 kb). The v + i method used for the library construction is
                described in detail in Smith, H. and Venter, J.C. (Making small
                insert libraries for whole genome shotgun sequencing projects. In
                Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                Barrell, Oxford University Press, 1999).
                Email: neilsayed@tigr.org
                Details of T. brucei sequencing at the Sanger Centre are available
                at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
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    1. .26
    /organism="Trypanosoma brucei"
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    /db_xref="taxon:5691"
    /clone="321g11"

Query Match      0.24; Score 16; DB 1; Length 26;
Best Local Similarity 79.24; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      4020 AAAAAAGAGAGAAAAAATAATGTT 4043
        ||||| ||||| ||||| |||||
Db      2 AAAAAAAAAAAAAAAAAAATTTT 25

RESULT 1273
AU265518/c      26 bp mRNA linear EST 10-MAY-2002
LOCUS          AU265518 VS Dictyostelium discoideum cDNA clone VSF623 5', mRNA
DEFINITION     sequence.
ACCESSION      AU265518
VERSION        AU265518.1  GI:20524316
KEYWORDS       EST.
SOURCE         Dictyostelium discoideum
ORGANISM       Dictyostelium discoideum
                Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
REFERENCE      1 (bases 1 to 26)
AUTHORS       Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Meeda,M.,
                Takeuchi,I., Kohara,Y. and Tanaka,Y.
                Population analysis of cDNAs from unicellular and multicellular
                stages of Dictyostelium discoideum
                Unpublished (2002)
TITLE         Contact: Hideko Urushihara
                Institute of Biological Sciences
                University of Tsukuba
                1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                Tel: 81-298-53-4664
                Fax: 81-298-53-6614
                Email: hideko@biol.tsukuba.ac.jp.
JOURNAL COMMENT
                Location/Qualifiers
FEATURES
  source
    1. .26
    /organism="Dictyostelium discoideum"

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/mol_type="mRNA"
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/clone="VSF623"
/sex="mat A"
/dev_stage="vegetative"
/clone_1ib="VS"

Query Match      0.24; Score 16; DB 1; Length 26;
Best Local Similarity 79.24; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      6977 AAAAAACAAACAGAAATGAGTGCG 7000
        ||||| ||||| ||||| |||||
Db      26 AAAAAAAAAAAAAAAAAAGCGGGG 3

RESULT 1274
R59382/c      27 bp mRNA linear EST 24-MAY-1995
LOCUS          R59382
DEFINITION     YH17607.81 Soares infant brain IN1B Homo sapiens cDNA clone
                IMAGE:37726 3', similar to gb:M5131 METHYLMALONYL-COA MUTASE
                PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION      R59382
VERSION        R59382.1  GI:830077
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 27)
AUTHORS       Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
                Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                Trevaaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
                Wilson,R.
                The WashU-Merck EST Project
                Unpublished (1995)
                Contact: Wilson RK
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                High quality sequence starts: 1
                High quality sequence stops: 1
                Source: IMAGE Consortium, LNLN
                This clone is available royalty-free through LNLN, contact the
                IMAGE Consortium (info@image.lnl.gov) for further information.
                Trace considered overall poor quality
                Possible reversed clone: polyT not found
                Seq primer: SP6
                High quality sequence stop: 1.
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    /lab_host="DH10B (ampicillin resistant)"
    /clone_1ib="Soares infant brain IN1B"
    /note="Organ: whole brain; Vector: Lfam1d BA; Site 1: Not
    I; Site 2: Hind III; 1st strand cDNA was primed with a Not
    I - oligo(dT) primer [5']
    AACTGGAAGATTCGGCGCGAGATTTTATTTTATTTT 3';
    double-stranded cDNA was ligated to Hind III adaptors
    (Pharmacia), digested with Not I and directionally cloned
    into the Not I and Hind III sites of the Lfam1d BA vector.
    Library went through one round of normalization. Library
    constructed by Bento Soares and M.Fatima Bonaldo."

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Query Match 0.2%; Score 16; DB 1; Length 27;  
 Best Local Similarity 79.2%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4016 TGAGAAAAAGAGAGAAAAA 4039  
 |||||  
 25 TGAAGAAAAAGAAAAA 2

RESULT 1275  
 CF298134/c 32 bp mRNA 1linear EST 15-AUG-2003  
 LOCUS  
 DEFINITION NACL--08-M01.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 ACCESSION CF298134  
 VERSION CF298134.1 GI:33669895  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source 1..32

/organism="Oryza sativa"  
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 /db\_xref="taxon:4530"  
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 /tissue\_type="callus"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 32;  
 Best Local Similarity 79.2%; Pred. No. 1.8e+03;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4016 TGAGAAAAAGAGAGAAAAA 4039  
 |||||  
 30 TGAAGAAAAAGAAAAA 7

RESULT 1276  
 CF298134/c 19 bp mRNA 1linear EST 15-AUG-2003  
 LOCUS  
 DEFINITION 7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 ACCESSION CF298134  
 VERSION CF298134.1 GI:33669895  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source 1..19

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--01-G09"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1ib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482  
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 19 TTTT TTTT TTTT TTTT CTT 1

RESULT 1277  
 CF298472

LOCUS CF298472 19 bp mRNA 1linear EST 15-AUG-2003  
 DEFINITION 7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 ACCESSION CF298472  
 VERSION CF298472.1 GI:33670233  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source 1..19

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--01-001"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1ib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for

## RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTCTTTTTTTTTTTT 4482  
|||||  
1 TTTTCTCTTTTTTTTTTTT 19

## RESULT 1278

AZ345499 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION 1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080F06 F, genomic survey sequence.

ACCESSION AZ345499  
VERSION AZ345499.1 GI:10424736

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Iellam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weise,R.

REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

University of Utah Genome Center  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: F column: 06  
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Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

## FEATURES

SOURCE

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1[4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTCTTTTTTTTTTTT 4482  
|||||  
1 TTTTCTCTTTTTTTTTTTT 19

## RESULT 1279

AZ509929 19 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION 1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0354A07 F, genomic survey sequence.

ACCESSION AZ509929  
VERSION AZ509929.1 GI:10691245

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Iellam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weise,R.

REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

University of Utah Genome Center  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: A column: 07  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

## FEATURES

SOURCE

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/organism="Mus musculus"  
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/clone="UUGC1M0354A07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1[4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."



Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTGT 4485  
 Db 19 TTTTCTTTTCTTTTGT 1

RESULT 1282  
 AZ786336 19 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0031H17R Mouse 10kb plasmid UGSC1M library Mus musculus genomic  
 DEFINITION Clone UGSC2M0031H17 R, genomic survey sequence.  
 ACCESSION AZ786336  
 VERSION AZ786336.1 GI:12923992  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0031 row: H column: 17  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGSC2M0031H17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGSC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi14732114|gb|AF129072.1)' a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTT 4482  
 Db 1 TTTTCTTTTCTTTTCTTTT 19

RESULT 1283  
 AM333777 20 bp mRNA linear EST 31-JAN-2000  
 LOCUS 525H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
 DEFINITION AM333777  
 ACCESSION AM333777  
 VERSION AM333777.1 GI:6830134  
 KEYWORDS EST.  
 SOURCE Pneumocystis carinii  
 ORGANISM Pneumocystis carinii  
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
 Pneumocystidaceae; Pneumocystis.  
 1 (bases 1 to 20)  
 Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
 Edman,J.C., Kovacs,J. and Cushion,M.  
 Expressed sequence tags from Pneumocystis carinii  
 Unpublished (2000)  
 JOURNAL Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY  
 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staben@pop.uky.edu.  
 Location/Qualifiers  
 1..20  
 /organism="Pneumocystis carinii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4754"  
 /lab\_host="E. coli"  
 /clone\_lib="AGS-1"  
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
 P. carinii organisms (3x10e9) from a single rat (99-1-6,  
 sacrificed on 3/17/99) at Cincinnati VA facilities.  
 Trizol extracted RNA. Oligo dt priming, standard  
 conditions described by vendor, Stratagene. Further  
 details see www.uky.edu/Project/pneumocystis/"

Query Match 0.2%; Score 15.8; DB 1; Length 20;  
 Best Local Similarity 89.5%; Pred. No. 9.5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 1284  
 CF331733 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--07-P15-b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION NACL--07-P15-b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--07-P15, mRNA sequence.  
 ACCESSION CF331733  
 VERSION CF331733.1 GI:33811693  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzoae; Oryza.  
 1 (bases 1 to 20)  
 Song,S.I., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Kim,J.S., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

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1. 20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL-07-P15"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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## Query Match

Best Local Similarity 0.2%; Score 15.8; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Qy

4460 GCACCTTTTCTTTTCTTTT 4478

## Db

19 GCGCTTTTCTTTTCTTTT 1

## RESULT 1285

AZ345710 20 bp DNA linear GSS 29-SRP-2000  
LOCUS AZ345710/c

DEFINITION 1M0080H05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080H05 R, genomic survey sequence.

ACCESSION AZ345710  
VERSION AZ345710.1 GI:10424947

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niedermaier, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: H column: 05  
Seq primer: CACACGAAACACGCTATGACC

Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source location/Qualifiers  
1. 20

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080H05"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## Query Match

Best Local Similarity 0.2%; Score 15.8; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Qy

4025 AGAGGAGAAACAAATGTT 4043

## Db

20 AGAGGAGAAACCTATGTT 2

## RESULT 1286

AZ313243 21 bp DNA linear GSS 29-SRP-2000  
LOCUS AZ313243

DEFINITION 1M0029H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0029H16 R, genomic survey sequence.

ACCESSION AZ313243  
VERSION AZ313243.1 GI:10357979

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niedermaier, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0029 row: H column: 16  
Seq primer: CACACGAAACACGCTATGACC

Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source location/Qualifiers  
1. 21

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0029H16"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3623 GGGTGGGGTGGAGAGCA 3641  
|||||  
Db 2 GGGTGTGGGTGGTGAAGA 20

#### RESULT 1287

AZ818565/c 21 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0088K10R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUCG2M0088K10 R, genomic survey sequence.

ACCESSION AZ818565  
VERSION AZ818565.1 GI:12988473

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiser,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

FEATURES  
source

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0088K10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: pMD2nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GGAATTTTTTTTTTTT 4478  
|||||  
Db 19 GGGGTTTTTTTTTTTTT 1

#### RESULT 1288

CF318882/c 22 bp mRNA linear EST 15-AUG-2003  
LOCUS CF318882  
DEFINITION HO-09-C23\_g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD-09-C23, mRNA sequence.

ACCESSION CF318882  
VERSION CF318882.1 GI:33690643

KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT Contact: Naim B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.

FEATURES  
source

1..22  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD-09-C23"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOP0, Site 1: EcoRI, Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY 5405 GCCATTCAAGATAATAAA 5423  
 Db 22 GCCATTCAAAAAAAAAAAAA 4

RESULT 1289  
 A2771221 23 bp DNA linear GSS 16-FEB-2001  
 LOCUS A2771221/c  
 DEFINITION 1M0573A16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0573A16 F, genomic survey sequence.  
 ACCESSION A2771221  
 VERSION A2771221.1 GI:12893248  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Niederhauser, A., and Wright, D., Weiss, R.  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished (2000)  
 JOURNAL University of Utah Genome Center  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0573 row: A column: 16  
 Seq primer: CGTTGTAACGACGCCACGACT  
 Class: plasmid ends

FEATURES  
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 location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UGCGIM0573A16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 23;  
 Best Local Similarity 89.5%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGACTTTTCTTTTCTTTT 4478

Db 19 GCGGTTTTTTTTTTTTTTT 1

RESULT 1290  
 A2314206 24 bp DNA linear GSS 29-SEP-2000  
 LOCUS A2314206  
 DEFINITION 1M0030H19R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0030H19 R, genomic survey sequence.  
 ACCESSION A2314206  
 VERSION A2314206.1 GI:10359866  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Niederhauser, A., and Wright, D., Weiss, R.  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished (2000)  
 JOURNAL University of Utah Genome Center  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0030 row: H column: 19  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends

FEATURES  
 source  
 location/Qualifiers  
 1..24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGIM0030H19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;  
 Best Local Similarity 89.5%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6004 GGAGGTTCTGGCATTTT 6022

Db 5 GGATGTTTCGACCTT 23

RESULT 1291  
AZ658569/c 24 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0535L19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0535L19 F, genomic survey sequence.  
ACCESSION AZ658569  
VERSION AZ658569.1 GI:11795715  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0535 row: L column: 19  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

FEATURES  
source 1..24  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0535L19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;  
Best Local Similarity 89.5%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4405 TTATCAAAATGATTTT 4423  
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Db 23 TTTAAAAAATGATTTAT 5

RESULT 1292  
AZ658569/c 24 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0535L19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0535L19 F, genomic survey sequence.  
ACCESSION AZ658569  
VERSION AZ658569.1 GI:11795715  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0535 row: L column: 19  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

FEATURES  
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/mol\_type="genomic DNA"  
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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;  
Best Local Similarity 89.5%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5086 TAACATCCATCGCCCTG 5104  
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Db 23 TCACACCCCATCGCCCTG 5

RESULT 1293  
 AM327923 27 bp mRNA linear EST 28-JAN-2000  
 LOCUS dr02908.x1 NIH\_MGC\_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA  
 DEFINITION sequence.  
 ACCESSION AM327923  
 VERSION AM327923.1 GI:6798418  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 27)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Edge Biosystems  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrrp/image/image.html  
 Place: LNCM0029 row: M column: 16  
 Seq primer: -21m3 forward primer (ABI).  
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 Edge Biosystems."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAGAAACAAA 4038  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1294  
 CF291968 27 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14RCOT--02-J21.b1 Rice root plasmid cDNA library (14RCOT) Oryza  
 DEFINITION sativa cDNA clone 14RCOT--02-J21, mRNA sequence.  
 ACCESSION CF291968  
 VERSION CF291968.1 GI:33661001  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriaroidae; Oryzaceae; Oryza.  
 1 (bases 1 to 27)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of BioScience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

FEATURES  
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 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
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 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAGAAACAAA 4039  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1295  
 CF299084 27 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--02-P02, mRNA sequence.  
 ACCESSION CF299084  
 VERSION CF299084.1 GI:33670845  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriaroidae; Oryzaceae; Oryza.  
 1 (bases 1 to 27)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of BioScience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAGAAACAAA 4039  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1296  
CF329725/c 27 bp mRNA linear EST 18-AUG-2003  
LOCUS  
DEFINITION NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
ACCESSION CF329725  
VERSION CF329725.1 GI:33807665  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.  
1 (bases 1 to 27)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4038  
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1297  
CF330557/c 27 bp mRNA linear EST 18-AUG-2003  
LOCUS  
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza  
ACCESSION CF330557  
VERSION CF330557.1 GI:33809352  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.  
1 (bases 1 to 27)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193

Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
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/lab\_host="E.coli DH10B"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4038  
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1298  
CF335229/c 27 bp mRNA linear EST 18-AUG-2003  
LOCUS  
DEFINITION JMT--04-N08.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--04-N08, mRNA sequence.  
ACCESSION CF335229  
VERSION CF335229.1 GI:33818810  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.  
1 (bases 1 to 27)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..27  
/organism="Oryza sativa"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
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prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4038



RESULT 1301  
 AZ486791/c 27 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0315K21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0315K21 F, genomic survey sequence.  
 ACCESSION AZ486791  
 VERSION AZ486791.1 GI:10653911  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0315 row: K column: 21  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGAAACAA 4038  
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 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1302  
 AZ511894/c 27 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0357E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0357E11 F, genomic survey sequence.  
 ACCESSION AZ511894  
 VERSION AZ511894.1 GI:10693210  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0357 row: E column: 11  
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 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0357E11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGAAACAA 4038  
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 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1303  
 AZ580921/c  
 LOCUS 27 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0369E24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0369E24 F, genomic survey sequence.  
 ACCESSION AZ580921  
 VERSION AZ580921  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0369 row: E column: 24  
 Seq primer: CCGTGTAAACGACGCCAGCT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATCGAGAAAAGAGAAACAA 4038  
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 DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1304

AZ616094/c  
 LOCUS 27 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0445E17R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0445E17 R, genomic survey sequence.  
 ACCESSION AZ616094  
 VERSION AZ616094  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0445 row: E column: 17  
 Seq primer: CACACAGAAACAGCATGACC  
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 High quality sequence stop: 27.  
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 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATCGAGAAAAGAGAAACAA 4038  
 |||||  
 DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1305  
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LOCUS A2623186 27 bp DNA linear GSS 13-DEC-2000  
 DEFINITION IM0460D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0460D12 R, genomic survey sequence.  
 ACCESSION A2623186  
 VERSION A2623186  
 KEYWORDS A2623186.1 GI:11745376  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0460 row: D column: 12  
 Seq primer: CACACAGAAAACGCTATGACC  
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 High quality sequence stop: 27.  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0460D12"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAAAACAA 4038  
 |||||  
 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1306  
 LOCUS A2627847/c 27 bp DNA linear GSS 13-DEC-2000  
 A2627847

DEFINITION IM0474011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0474011 F, genomic survey sequence.  
 ACCESSION A2627847  
 VERSION A2627847  
 KEYWORDS A2627847.1 GI:11750133  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0474 row: O column: 11  
 Seq primer: CGTTGTAACGACGCGCAGT  
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 High quality sequence stop: 27.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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 /note="Vector: PWD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAAAACAA 4038  
 |||||  
 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1307  
 LOCUS A2809295 27 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0073B1SF Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 A2809295



ACCESSION	clone UNGC2M0073B15 F, genomic survey sequence.				
VERSION	A2809295				
KEYWORDS	A2809295.1 GI:12975450				
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright D., Weise,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0073 Row: B Column: 15 Seq primer: CGTGTAAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 27.				
FEATURES	Location/Qualifiers				
SOURCE	1. 27 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UNG2M0073B15" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-" /clone_idb="Mouse 10kb plasmid UNG2M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
Query Match	0.24;	Score 15.8;	DB 1;	Length 27;	
Best Local Similarity	74.11;	Pred. No. 1.66+03;			
Matches	20;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Oy	4012	AAATGAGAAAAAGAGAGAAACAA	4038		
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAA	27		
RESULT 1308					
LOCUS	TA355B06P	27 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic clone 355b06, forward sequence, genomic survey sequence.				

ACCESSION	AL493923	GI:11870552
VERSION	GSS.1.1	
KEYWORDS	Trypanosoma brucei	
SOURCE	Trypanosoma brucei	
ORGANISM	Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;	
REFERENCE	1 (bases 1 to 27)	
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.	
TITLE	Submitted (10-DGC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk	
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	
FEATURES	Email: nh@sanger.ac.uk Details of T. brucei sequencing at the Sanger Centre are available at <a href="http://www.sanger.ac.uk/Projects/T_brucei/">http://www.sanger.ac.uk/Projects/T_brucei/</a> .	
SOURCE	location/Qualifiers	
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Query Match	0.2%;	Score 15.8; DB 1; Length 27;
Best Local Similarity	74.1%;	Pred. No. 1.6e+03;
Matches	20; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
Db	4012	AAAAATGAGAAAAAGAGAAAAACAA 4038
	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 27
RESULT 1309		
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LOCUS	AZ941721	27 bp DNA linear GSS 26-APR-2001
DEFINITION	2M02010I04R Mouse 10kb plasmid tUGC2M library Mus musculus genomic clone UGC2M02010I04 R, genomic survey sequence.	
ACCESSION	AZ941721	
VERSION	AZ941721	
KEYWORDS	AZ941721.1 GI:13804440	
SOURCE	GSS.	
ORGANISM	Mus musculus (house mouse)	
	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 27)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SVC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu	

Insert Length: 10000 Std Error: 0.00  
Plate: 0201 row: 0 column: 04  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

## FEATURES

Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1fb="Mouse 10kb plasmid UGCG2M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAGAGAACAA 4038  
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 1310

AZ434285

LOCUS 27 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0220B08R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0220B08 R, genomic survey sequence.

ACCESSION

AZ434285

AZ434285.1 GI:10558298

GSS.

Mus musculus (house mouse)

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0220 row: B column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

## FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone\_1fb="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAGAGAACAA 4038  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 27

## RESULT 1311

AZ458228

LOCUS 27 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0262C12F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0262C12 F, genomic survey sequence.

ACCESSION

AZ458228

AZ458228.1 GI:10616353

GSS.

Mus musculus (house mouse)

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0262 row: C column: 12

Seq primer: CGTGTGTAAGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers

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1. 27  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U06C1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1312  
 AL048439 28 bp mRNA linear EST 04-SEP-2003  
 LOCUS DKFZP586I1924\_r1 586 (synonym: hute1) Homo sapiens cDNA clone  
 DEFINITION DKFZP586I1924, mRNA sequence.  
 ACCESSION AL048439  
 VERSION AL048439  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 28)  
 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 EST (Duesterhoeft, et al.)  
 Unpublished (1999)  
 JOURNAL CONTACT: MIPS  
 COMMENT MIPS  
 FEATURES  
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 Location/Qualifiers  
 1. 28  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZP586I1924"  
 /issue\_type="uterus"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="586 (synonym: hute1)"  
 /note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI/MluI"

Query Match  
 Best Local Similarity 74.1%; Pred. No. 1.7e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1313  
 CF322082/c 28 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD-13-123.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION HD-13-123.g1 Oryza sativa cDNA clone HD-13-123, mRNA sequence.  
 ACCESSION CF322082  
 VERSION CF322082  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 28)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nam, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)  
 CONTACT: Nam, B.H.  
 Genomic and Genetic Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnamh@gbio.com, bnamh@bio.myongji.ac.kr.  
 FEATURES  
 source  
 Location/Qualifiers  
 1. 28  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match  
 Best Local Similarity 74.1%; Pred. No. 1.7e+03;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1314  
 CF337400 28 bp mRNA linear EST 18-AUG-2003  
 LOCUS JMT--07-N04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA  
 DEFINITION JMT--07-N04.g1 Oryza sativa cDNA clone JMT--07-N04, mRNA sequence.  
 ACCESSION CF337400  
 VERSION CF337400.1 GI:33823200  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

FEATURES  
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1. .28  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT-07-N04"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
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/clone\_lib="AluMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: PCR4-NOPO, Site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonic Acid Carboxyl  
methyltransferase overexpression line."

Query Match  
Best Local Similarity 74.1%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4011 TAAATGAGAAAAAGAGAAACAA 4037  
Db 2 TAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1315  
AZ481286/c 28 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0303124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0303124 F, genomic survey sequence.  
ACCESSION AZ481286.1 GI:10642351  
VERSION GSS.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0303 row: L column: 24  
Seq primer: CATTGTAAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 28.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
Location/Qualifiers  
1. .28  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1472114[gp]A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match  
Best Local Similarity 74.1%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4010 CTAAATGAGAAAAAGAGAAACCA 4036  
Db 28 CAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1316  
TS6352/c 28 bp mRNA linear EST 06-FEB-1995  
LOCUS y34c09.g1 Stratagene fetal spleen (#937205) Homo sapiens cDNA  
DEFINITION clone IMAGE:73072.3' similar to gp:541458 ROD  
CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN),  
mRNA sequence.  
ACCESSION TS6352  
VERSION TS6352.1 GI:658213  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,  
Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W.,  
Hawkins, M., Huilman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
Rohtling, T., Schellberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
Trevaekis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.  
and Maria, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1

**DNA**

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1. 29
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/strain="C57BL/6J"
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/clone="UTGCG2M0100N08"
/sex="Male"
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/cultivar="KMS320 (double haploid, monogerm breeding
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Db	4012	AAATGAGAAAAAGAGAAAAACAA	4038	
	27	AAAAAAAAACAAAAAAAAAAAAACA	1	
RESULT 1319				
LOCUS	BX554779/c	30 bp	mRNA	linear
DEFINITION	BX554779	Glossina morsitans morsitans adult infected gut	Glossina	EST 10-OCT-2003
ACCESSION	BX554779	morsitans cDNA clone Tse17d12_p1c		mRNA sequence.
VERSION	BX554779.1	GI:33378835		
KEYWORDS	EST.			
SOURCE	Glossina morsitans morsitans			
ORGANISM	Glossina morsitans morsitans			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pretygota;			
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
	Hippoboscidea; Glossinidae; Glossina.			
REFERENCE	1 (bases 1 to 30)			
AUTHORS	Lehane, M. J., Akasy, S., Gibson, W., Kerhornou, A., Berriman, M.,			
	Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.			
	Adult midgut expressed sequence tags from the tsetse fly Glossina			
	morsitans morsitans and expression analysis of putative immune			
	response genes			
	Genome Biol. 4 (10), R63 (2003)			
JOURNAL	22881942			
MEDLINE	14519198			
PUBMED				
COMMENT	Contact: Hall N			
	Pathogen Sequencing Unit			
	The Sanger Institute The Wellcome Trust Genome Campus			
	Hinxton, Cambridge, CB10 1SA, UK			
	Request for clones, please contact: Mike Lehane			
	Prof. M. J. Lehane			
	School of Biological Sciences,			
	University of Wales,			
	Bangor LL57 2UW			
	All clones with suffix q1c are reverse primer reads starting at 5'			
	end of the cDNA all p1c reads are from			
	the 3' end.			
FEATURES	Location/Qualifiers			
source	1..30			
	/organism="Glossina morsitans morsitans"			
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	/tissue_type="adult infected gut"			
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	/note="country: Zimbabwe; EST from adult gut infected with			
	T.brucei"			
Query Match	0.2%	Score 15.8	DB 1	Length 30
Best Local Similarity	74.1%	Pred. No. 1.8e+03		
Matches	20	Conservative	0	Mismatches 7; Indels 0; Gaps 0;
4018	AGAAAAAGAGAAAAAATAATGTTA	4044		

Db	30	AAAAAAAAAAAAAAAAAACTTTTA	4
RESULT	1320		
LOCUS	AZ326012		
DEFINITION	AZ326012	32 bp DNA	linear GSS 29-SEP-2000
ACCESSION	U00048A19	Mouse 10kb plasmid UGCGIM library	Mus musculus genomic
VERSION	clone UGCGIM0048A19	R, genomic survey sequence.	
KEYWORDS	AZ326012		
SOURCE	AZ326012.1	GI:10383271	
ORGANISM	Mus musculus	(house mouse)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 32)		
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,		
	Tellam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,		
	Relly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von		
	Niederhausern, A. and Wright, D., Weis, R.		
	Mouse whole genome scaffolding with paired end reads from 10kb		
	plasmid inserts		
	Unpublished (2000)		
	Contact: Robert B. Weiss		
	University of Utah Genome Center		
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		
	84112, USA		
	Tel: 801 585 5606		
	Fax: 801 585 7177		
	Email: ddunn@genetics.utah.edu		
	Insert Length: 10000	Std Error: 0.00	
	Plate: 0048	row: A column: 19	
	Seq primer: CACACAGAAAACACTATGACC		
	Class: plasmid ends		
	High quality sequence stop: 32.		
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	/sex="Male"		
	/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"		
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	/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson		
	Laboratory Mouse DNA Resource		
	(http://www.jax.org/resources/documents/dnares/). The DNA		
	was hydrodynamically sheared by repeated passage through a		
	0.005 inch orifice at constant velocity. The sheared DNA		
	was blunt end-repaired with T4 DNA polymerase and T4		
	polynucleotide kinase. Adaptor oligonucleotides were		
	ligated to the blunt ends in high molar excess. The		
	adapted DNA was purified and size-selected for a 9.5 to		
	10.5 kb range using preparative agarose gel		
	electrophoresis. Vector DNA was prepared from a derivative		
	of PMD42 [G14732114 gb AF129672.1], a copy-number		
	inducible derivative of plasmid R1. The vector was ligated		
	with adaptors complementary to the insert adaptors and		
	purified. The sheared, adapted mouse DNA was annealed to		
	adapted vector DNA, and transformed into		
	chemically-competent E. coli XL10-Gold (Stratagene) cells		
	and selected for ampicillin resistance."		
Query Match	0.2%	Score 15.8	DB 1; Length 32;
Best Local Similarity	74.1%	Pred. No. 1.9e+03;	
Matches	20;	Conservative 0;	Mismatches 7; Indels 0; Gaps 0;
4013	AAATGACAAAAAGAGACAAACAAA	4039	

Db 5 AACCAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 1321  
TA264B08P 38 bp DNA linear GSS 13-DEC-2000  
LOCUS TA264B08P/c  
DEFINITION T. brucei sheared genomic DNA clone 264b08, forward sequence,  
genomic survey sequence.  
ACCESSION AL483993  
VERSION AL483993.1 GI:11849953  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE  
AUTHORS 1 (bases 1 to 38)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
1..38  
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/mol\_type="genomic DNA"  
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Query Match 0.2%; Score 15.8; DB 1; Length 38;  
Best Local Similarity 74.1%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAAACA 4038  
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAA 12

RESULT 1322  
A2770047 42 bp DNA linear GSS 16-FEB-2001  
LOCUS A2770047/c  
DEFINITION 1M0571B19F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0571B19 F, genomic survey sequence.  
ACCESSION A2770047  
VERSION A2770047.1 GI:12890825  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 42)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0571 row: B column: 19  
Seq primer: CGTTCGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 42.  
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/clone="UGCLM0571B19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 42;  
Best Local Similarity 65.7%; Pred. No. 1.8e+03;  
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2459 GCAGCAGCAGCAGCATCCAGGCGACCGCCGACCA 2493  
Db 42 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 8

RESULT 1323  
TA303G05P 22 bp DNA linear GSS 13-DEC-2000  
LOCUS TA303G05P/c  
DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence,  
genomic survey sequence.  
ACCESSION AL497383  
VERSION AL497383.1 GI:11865504  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE  
AUTHORS 1 (bases 1 to 22)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

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/clone="303g05"
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Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGACAAACAAA 4039  
1 AAAAAAAAAAGAAAAAAA 22

## RESULT 1324

AA999803 22 bp mRNA linear EST 05-JUN-1998  
LOCUS 0641d04.61 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1607911.3,  
DEFINITION similar to TR:Q34192 Q34192 NADH DEHYDROGENASE SUBUNIT 5., mRNA  
sequence.

ACCESSION AA999803.1 GI:3190358  
VERSION AA999803  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 22)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILMNI at:  
[www-bio.lnlnl.gov/bbrp/image/image.html](http://www-bio.lnlnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

## source

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1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1607911"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_11b="NCI CGAP Br2"
/notes="Vector: pT7T3D-Pac (pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from pooled bulk
```

breast tumor tissue, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. This library is the normalized version of  
NCI CGAP Br1.1. Library was constructed by Bento Soares  
and M. Fatima Bonaldo."

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4464 TTTTGTGTGTGTGTGTGTGTGT 4485  
1 TTTTGTGTGTGTGTGTGTGTGT 22

## RESULT 1325

CF300339 22 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--04-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--04-L05, mRNA sequence.

ACCESSION CF300339.1 GI:33672100  
VERSION CF300339.1  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6355  
Fax: 82 31 321 6193  
Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

## FEATURES

## source

```
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-L05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_11b="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
```

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4466 TTTTGTGTGTGTGTGTGTGTGT 4487  
1 TTTTGTGTGTGTGTGTGTGTGT 22

## RESULT 1326

AZ471736 22 bp DNA linear GSS 04-OCT-2000  
LOCUS IM0286112R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M0286112 R, genomic survey sequence.

ACCESSION AZ471736  
VERSION AZ471736.1 GI:10629957



KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0286 row: 1 column: 12  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source  
1. 22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0286112"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4462 ACCTTTTATGCTTTT 4483  
DB 22 ATTATTTATGCTTTT 1

RESULT 1327  
AZ592068/c 22 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0402H08R Mouse 10kb plasmid UGCIM library Mus musculus genomic  
ACCESSION AZ592068  
VERSION AZ592068.1 GI:11714258  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0402 row: H column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

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1. 22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0402H08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7443 GGTGTTTAAAGACACAGTG 7464  
DB 22 GTGTTGGCAATACACAGTG 1

RESULT 1328  
AZ633751 22 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M048911F Mouse 10kb plasmid UGCIM library Mus musculus genomic  
ACCESSION AZ633751  
VERSION AZ633751.1 GI:11755941  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: 1 column: 11  
Seq primer: CTTCTTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0489111"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5327 TCTCTCTTTGCTCTCTCTC 5348  
Db 1 TCTCTCTCTCTCTCTCTCTC 22

RESULT 1329  
LOCUS TAI89G04P/c 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 189g04, forward sequence,  
genomic survey sequence.  
ACCESSION AL477750.1 GI:11841701  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)  
AUTHORS Hall,N., Bowman,S., Leonard,N.J., Doggett,J., Ackin,R., Chillingworth,C., Ormond,D., Harrie,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1. .22  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="189g04"

Query Match 0.2%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5318 CTCTCTTTTCTCTCTTTGCTT 5339  
Db 22 CTCTCTTTGCTCTTTTGCT 1

RESULT 1330  
LOCUS A2486853/c 23 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0315M1R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0315M14 R, genomic survey sequence.  
ACCESSION A2486853  
VERSION A2486853.1 GI:10654033  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: M column: 14  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

source

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGCM0315M14"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 81.8%; Score 15.6; DB 1; Length 23;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

4018 AGAAAAAGAGAGAAAAACAAA 4039

Db

23 AAAAAAAAAAGAGAAAAAAA 2

RESULT 1331

A2645254/C

LOCUS

DEFINITION 23 bp DNA linear GSS 14-DEC-2000

1M0510005R Mouse 10kb plasmid UGGCM library Mus musculus genomic

clone UGGCM0510005 R, genomic survey sequence.

ACCESSION A2645254

VERSION A2645254.1 GI:11774572

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Iseim,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0510 Row: O Column: 05

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

source

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGCM0510005"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 81.8%; Score 15.6; DB 1; Length 23;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

4018 AGAAAAAGAGAGAAAAACAAA 4039

Db

23 AAAAAAAAAAGAGAAAAAAA 2

RESULT 1332

AU012506/C

LOCUS

DEFINITION 23 bp mRNA linear EST 03-AUG-1998

AU012506 Schizosaccharomyces pombe late log phase cDNA

Schizosaccharomyces pombe cDNA clone spc06850, mRNA sequence.

ACCESSION AU012506

VERSION AU012506.1 GI:3357415

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

1 (bases 1 to 23)

Moriyomo,M. and Mita,K.

Identification of expressed sequence tags of Schizosaccharomyces

pombe

Unpublished (1998)

Contact: Mitsuo Moriyo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 265-8555, Japan

Email: moriyomo@nirs.go.jp.

Location/Qualifiers

1..23

/organism="Schizosaccharomyces pombe"

/mol\_type="mRNA"

/strain="972"

/db\_xref="taxon:4896"

/clone="spc06850"

/sex="h minus"

/clone\_lib="Schizosaccharomyces pombe late log phase cDNA"

/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA

sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nhrs.go.jp>)"

Query Match 0.2%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4027 AGAGAAACAAATGTTATTTT 4049  
Db 23 AGAGATTAAGTTATTTT 1

# RESULT 1333 AZ618720/c

LOCUS 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0450019 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0450019 F, genomic survey sequence.

ACCESSION AZ618720  
VERSION AZ618720.1 GI:11740826

## KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0450 row: O column: 19  
Seq primer: CTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

### source

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0450019"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 81.8%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3622 GGGGTGGGGTGGGAGAGAGAG 3643  
Db 23 GGGGGGGGGGGGGGGGAGG 2

# RESULT 1334 AZ793326/c

LOCUS 23 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0046B04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0046B04 R, genomic survey sequence.

ACCESSION AZ793326  
VERSION AZ793326.1 GI:12938168

## KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0046 row: B column: 04  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

### source

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0046B04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 81.8%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGAGAGAGG 3643  
|||||  
Db 22 GGGGTGGGGTGGGGGGGGG 1

# RESULT 1335

AZ822888 23 bp DNA linear GSS 20-FEB-2001  
LOCUS AZ822888/c

DEFINITION 2M0265123F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0096G06 R, genomic survey sequence.

ACCESSION AZ822888

VERSION AZ822888.1 GI:12992796

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contract: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0096 row: G column: 06

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0096G06"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1) a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 81.8%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5327 TCTCTCTTGGCTACTCTCTC 5348  
|||||  
Db 22 TCTCTCTCTCTCTCTCTC 1

# RESULT 1336

AZ984045 23 bp DNA linear GSS 27-APR-2001  
LOCUS AZ984045

DEFINITION 2M0265123F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0265123 F, genomic survey sequence.

ACCESSION AZ984045

VERSION AZ984045.1 GI:13852272

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contract: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0265 row: I column: 23

Seq primer: CGTGTAAACAGCAGCCAGCT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0265123"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1) a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."



JOURNAL  
COMMENT

Unpublished (1999)  
Other ESTs: 2821537.Sprime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing project  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 24 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LICM7 row: B column: 2  
High quality sequence stop: 14.  
Location/Qualifiers

## FEATURES

## source

1. .24  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821537"  
/issue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH\_MGC\_7"  
/note="Organ: Lung; Vector: POTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## Query Match

Best Local Similarity 0.2%; Score 15.6; DB 1; Length 24;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4476 TTTTTCCTTGTGACATCG 4497  
|||||

Db 1 TTTTTCCTTGTGACATCG 22  
|||||

RESULT 1340  
AW248929/c 24 bp mRNA linear EST 07-JAN-2000  
LOCUS  
DEFINITION  
2819212.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819212 3', mRNA sequence.  
ACCESSION  
AW248929  
VERSION  
AW248929.1 GI:6591922  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
COMMENT  
Unpublished (1999)  
Other ESTs: 2819212.Sprime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing

## FEATURES

## source

project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 10 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 24 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LICM1 row: A column: 5  
High quality sequence stop: 10.  
Location/Qualifiers

## Query Match

Best Local Similarity 0.2%; Score 15.6; DB 1; Length 24;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGAGAGAAACAAA 4039  
|||||

Db 24 AGAAAAAGAGAGTAAACAAA 3  
|||||

RESULT 1341  
AZ404465 24 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION  
1M0172P09R Mouse 10kb plasmid UNGCM library Mus musculus genomic clone UNGCM0172P09 R, genomic survey sequence.  
ACCESSION  
AZ404465  
VERSION  
AZ404465.1 GI:10528394  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0172 row: P column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

## FEATURES

## source

1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0172P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 24;  
Best Local Similarity 81.8%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3622 GGGGTGGGGGTGGAGAGAGAG 3643  
Db 2 GGGGGGGGGGAGAGAGAGGGG 23

RESULT 1342  
AZ404078 25 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M017207F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M017207 F, genomic survey sequence.  
ACCESSION AZ404078  
VERSION AZ404078.1 GI:10528091  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0172 row: J column: 07

Seq primer: CGTTGTAAAGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

## FEATURES

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1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M017207"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 25;  
Best Local Similarity 81.8%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4018 AGAAAAAGAGAGAAACAAA 4039  
Db 4 AAAAAAAAAAGAAAAAAAAA 25

RESULT 1343  
AM249476/c 25 bp mRNA linear EST 07-JAN-2000  
LOCUS 2821131.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821131 3',  
DEFINITION mRNA sequence.  
ACCESSION AM249476  
VERSION AM249476.1 GI:6592469  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 25)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821131.Sprime  
CONTACT: Robert Strauberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNU) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNU at:  
[www-bio.llnl.gov/bdrp/image/image.html](http://www-bio.llnl.gov/bdrp/image/image.html) Base Calling / Quality  
Scores: PHRD from University of Washington Genome Center  
Trimming: cross match from University of Washington Genome Center  
PHRD suite. Poly-P identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 25  
contiguous PHRD high quality bases following vector sequence. Very



Low Quality Sequence: Trace file contained 25 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1C6 row: A column: 4  
High quality sequence stop: 25.

## FEATURES

## source

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1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821131"
/tissue_type="small cell carcinoma"
/cell_line="WGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC-7"
/note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match  
Best Local Similarity 81.8%; Score 15.6; DB 1; Length 25;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAGAAAAA 4039

Db 23 AAAAAAAAAAATAAAAAAAAA 2

RESULT 1344  
LOCUS A2635695/c

DEFINITION 26 bp DNA linear GSS 13-DEC-2000  
1M0493G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0493G18 F, genomic survey sequence.

ACCESSION A2635695  
VERSION A2635695.1 GI:11757885

## KEYWORDS

## SOURCE

GSS.  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

## FEATURES

## source

```
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: G column: 18
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
```

/db\_xref="taxon:10090"  
/clone="UUGC1M0493G18"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match  
Best Local Similarity 81.8%; Score 15.6; DB 1; Length 25;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAGAAAAA 4039

Db 26 AAAAAAAAAAAGAAAAAAAAA 5

RESULT 1345  
LOCUS CF298133/c

DEFINITION 27 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-G09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-G09, mRNA sequence.

ACCESSION CF298133  
VERSION CF298133.1 GI:33669894

## KEYWORDS

## SOURCE

## ORGANISM

## Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

## JOURNAL

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

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1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-G09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Query Match 0.2%; Score 15.6; DB 1; Length 27;  
 Best Local Similarity 81.8%; Pred. No. 1.7e+03;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039  
 |||||  
 Db 26 AGAAAAAGAGAAACAAA 5

RESULT 1346  
 AL587570/c 32 bp mRNA linear EST 02-MAR-2001  
 LOCUS AL587570 BP Chicken Brain Library Gallus gallus cDNA clone  
 DEFINITION ROS059809, mRNA sequence.  
 ACCESSION AL587570  
 VERSION AL587570.1 GI:13192604  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 32)  
 AUTHORS Murray, F.  
 TITLE BP Chicken Brain Library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Frazer Murray  
 Dept. Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UK  
 Tel: +44 (0)131 527 4200  
 Fax: +44 (0)131 440 0434  
 Email: frazer.murray@bbsrc.ac.uk  
 GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech  
 (\*6854-  
 Seq primer: M13F.  
 FEATURES  
 source 1..32 Location/Qualifiers  
 /organism="Gallus gallus"  
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 /db\_xref="taxon:9031"  
 /clone="ROS059809"  
 /tissue\_type="Brain"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B"  
 /clone\_lib="BP Chicken Brain Library"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned  
 unidirectionally. Primer: Oligo dT. 5' adaptor sequence:  
 5' TGACCTCGAG 3' ; 3' adaptor sequence: 5'  
 GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from  
 Clontech (\*6854-1)"

Query Match 0.2%; Score 15.6; DB 1; Length 32;  
 Best Local Similarity 81.8%; Pred. No. 1.9e+03;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039  
 |||||  
 Db 25 AGAAAAAGAGAAACAAA 4

RESULT 1347  
 BX556508/c 35 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX556508 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse27F04\_p1c, mRNA sequence.  
 ACCESSION BX556508  
 VERSION BX556508.1 GI:33427768  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhournou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix plc are reverse primer reads starting at 5'  
 end of the cDNA all plc reads are from  
 the 3' end.  
 FEATURES  
 source 1..35 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse27F04\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T. Brucei"

Query Match 0.2%; Score 15.6; DB 1; Length 35;  
 Best Local Similarity 81.8%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039  
 |||||  
 Db 32 AGAAAAAGAGAAACAAA 11

RESULT 1348  
 BX531095/c 37 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX531095 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse127c07\_p1c, mRNA sequence.  
 ACCESSION BX531095  
 VERSION BX531095.1 GI:33377293  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossiniidae; Glossina.  
 REFERENCE 1 (bases 1 to 37)  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhournou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane



Query Match 0.2%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
 |||||  
 1 TTTT TTTT TTTT TTTT TTTT 17

## RESULT 1351

BO591588

17 bp mRNA linear EST 06-DEC-2002

LOCUS BO12616-024-017-C15-SP6 MP12-ADIS-024-storage root Beta vulgaris

DEFINITION cDNA clone 024-017-C15 5-PRIME, mRNA sequence.

ACCESSION BO591588

VERSION BO591588.1 GI:26121171

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehnach, H.  
 and Radeloff, U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

JOURNAL

MEDLINE

PUBMED

12472698

COMMENT

Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpik-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 17 row: C column: 15  
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.  
 Location/Qualifiers

FEATURES

source

1. .17  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KMS2320 (double haploid, monogerm breeding  
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 /clone="024-017-C15"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_id="MP12-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
 |||||  
 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1352  
 CF276637/c  
 LOCUS 17 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF276637

VERSION CF276637.1 GI:33654023

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES

source

1. .17  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
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 /clone="14ETL--01-N18"  
 /tissue\_type="leaf"  
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 (14ETL)"  
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480  
 |||||  
 17 TTTT TTTT TTTT TTTT TTTT 1

## RESULT 1353

CF291802

17 bp mRNA linear EST 14-AUG-2003

LOCUS 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza

DEFINITION cDNA clone 14ROOT--02-G05, mRNA sequence.

ACCESSION CF291802

VERSION CF291802.1 GI:33660835

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193

Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## Bouyce

```

1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT-02-G05"
/rissue_type="root"
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/note="vector: pCR4-TOPO, Site_1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.2%	Score 15.4	DB 1	length 17
Best Local Similarity	94.1%	Pred. No. 7.8e+02		
Matches 16; Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	4464	TTTTTTTTTTTTTTTT	4480
Db	1	TGTTTTTTTTTTTTTT	17

**RESULT 1354**

LOCUS	CE299399	17 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	7LEAF--04-D19_b1 Rice leaf plasmid cDNA library II (7LEAF)				Oryza
DESCRIPTION	sativa cDNA clone 7LEAF--04-D19, mRNA sequence.				

**SOURCE**  
**ORGANISM**

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE	1 (cases 1 to 17)
AUTHORS	Kim J.S., Jun K.M., Cheong P.J., Kim M.J., Lee T.H., Shin Y.C.
TITLE	Song S.I., Kim J.K., Kim Y.-K., and Nahm B.H. Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.

## FEATURES

**Bourse**

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/organism="Oryza sativa"
/mol_type="mRNA"
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/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="rice leaf cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.2%	Score 15.4;	DB 1;	Length 17;
Best Local Similarity	94.1%;	Pred. No. 7.8e+02;		
Matches 16; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

[illegible]

**RESULT 1355**

LOCUS CF319075 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--09-H06.g1 OsHDA1C1-overexpressing transgenic rice plasmid cDNA  
FEATURES  
library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.

ACCESSION	CF319075	GI:33690836
VERSION	CF319075.1	
KEYWORDS	EST.	

SOURCE ORGANISM

REFERENCE  
1 (pages 1 to 17)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 17)	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.	Large-scale Sequencing Analysis of Rice ESTs	Unpublished (2003)	Contact: Nahm B.H.

## FEATURES

## Source

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1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHAKI-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR-TOPO, Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match	0.2%	Score 15.4	DB 1	Length 17
Best Local Similarity	94.1%	Pred. No. 7.8e+02		
Matches 16	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	4464	TTTTTTTTTTTTTTTTTTTT	4480
Db	1	TTTTTTTTTTTTTTTTTAT	17

**RESULT 1356**

LOCUS	CF329285	18 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza				
DESCRIPTION	sativa cDNA clone NACL--04-122, mRNA sequence.				
ACCESSION	CF329285				

**SOURCE ORGANISM**

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE AUTHORS	TITLE JOURNAL	COMMENT
1 (pages 1 to 18) Kim, S. I., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.	Large-scale Sequencing Analyses of Rice ESTs	Unpublished (2003) Contact: Nahm B. H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES  
source  
1. .18  
/organism="Oryza sativa"  
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/db\_xref="taxon:4530"  
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/issue\_type="callus"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1357  
CF326845/c 19 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--01-B12, mRNA sequence.  
ACCESSION CF326845  
VERSION CF326845.1 GI:33801944  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES  
source  
1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 19 TTTT TTTT TTTT TTTT TTTT 3

RESULT 1358  
A2447251 19 bp DNA linear GSS 04-OCT-2000  
LOCUS IM0244J19F Mouse 10kb plasmid UGCM library Mus musculus genomic  
DEFINITION clone UGCM0244J19 F, genomic survey sequence.  
ACCESSION A2447251  
VERSION A2447251.1 GI:10599050  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Niederhauser,A. and Wright,D.,Weiss,R., Tingey,A., von

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: J column: 19

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES  
source  
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/db\_xref="taxon:10090"  
/clone="UGCM0244J19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473214]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4480  
 Db 1 TTTT TTTT TTTT TTTT 17

RESULT 1359  
 AZ316368/c  
 LOCUS  
 DEFINITION 20 bp DNA linear GSS 29-SEP-2000  
 1M0034122F Mouse 10kb plasmid UGCGM1 library Mus musculus genomic  
 clone UGCGM0034122 F, genomic survey sequence.

ACCESSION  
 AZ316368  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0034 row: L column: 22  
 Seq primer: CATTCTTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
 source  
 Location/Qualifiers  
 1..20

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGM0034122"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UGCGM1 library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 4462 ACCTTTT TTTT TTTT 4478

Db 17 TTTT TTTT TTTT TTTT 1

RESULT 1360  
 AZ369092/c  
 LOCUS  
 DEFINITION 20 bp DNA linear GSS 02-OCT-2000  
 1M0119E01R Mouse 10kb plasmid UGCGM1 library Mus musculus genomic  
 clone UGCGM0119E01 R, genomic survey sequence.

ACCESSION  
 AZ369092  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0119 row: E column: 01  
 Seq primer: CACACAGAAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

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 Location/Qualifiers  
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/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGM0119E01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UGCGM1 library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3338 TTCAGATTCAGTTGT 3354

Db 19 TTAGATCCAGTTGT 3

RESULT 1361

CF330439 21 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa cDNA clone NACL--06-C12, mRNA sequence.

ACCESSION CF330439

VERSION CF330439.1 GI:33809110

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..21

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL--06-C12"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2M6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4480

|||||

Db 1 TTTT TTTT TTTT TTTT TTTT 17

|||||

RESULT 1362

AZ831993 21 bp DNA linear GSS 20-FEB-2001

LOCUS AZ831993

DEFINITION 2M0112M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112M01 F, genomic survey sequence.

ACCESSION AZ831993

VERSION AZ831993.1 GI:13001901

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: M column: 01

Seq primer: CCTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0112M01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydroynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7413 CAGCAGCAGCAGCAGCA 7429

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Db 5 CAGCAGCAGCAGCAGCA 21

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RESULT 1363

AZ843343 21 bp DNA linear GSS 20-FEB-2001

LOCUS AZ843343

DEFINITION 2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142K10 F, genomic survey sequence.

ACCESSION AZ843343

VERSION AZ843343.1 GI:13013251

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center



University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0142 row: K column: 10  
Seq primer: CATTGTAAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 21.

## FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0142K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/
/clone_lib="Mouse 10kb plasmid UGCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match  
Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4470 TTTTTCCTTC 4486  
Db 1 TTTTTCCTTC 17

RESULT 1364  
TA154D03P/C 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 154d03, forward sequence.  
ACCESSION AL472971 GI:11838244  
VERSION AL472971.1 GI:11838244  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 25)

## REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA, E-mail: barrrell@sanger.ac.uk and nhls@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

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1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="154d03"
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Query Match  
Best Local Similarity 76.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGACGAAACAAATGT 4042  
Db 25 AAAAAAAAAAAAAAAAAAAAAATTT 1

## RESULT 1365

A2764498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Niederhauser, A., and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: K column: 04

Seq primer: CACACGAAACGACTATGACC

Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0560K04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/
/clone_lib="Mouse 10kb plasmid UGCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
```

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA, E-mail: barrrell@sanger.ac.uk and nhls@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 25;  
Best Local Similarity 76.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 4024 AAGAGAGAAACAAATGTTATT 4048  
DB 1 AAAAAAAAAAAAAAAAAATTTTTT 25

## RESULT 1366

CF299646 26 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--03-L24, mRNA sequence.  
ACCESSION CF299646  
VERSION CF299646.1 GI:33671407  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
LOCATION/Qualifiers

## SOURCE

1..26  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/culivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--03-L24"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 26;  
Best Local Similarity 76.0%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 4015 ATGAGAGAGAGAGAGAGAGAG 4039  
DB 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1367  
TA236D08P 26 bp DNA linear GSS 13-DEC-2000  
LOCUS T1236D08P  
DEFINITION T. brucei sheared genomic DNA clone 236d08, forward sequence,  
genomic survey sequence.  
ACCESSION AL482943  
VERSION AL482943.1 GI:11647403  
KEYWORDS GSS.

SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE Hall N., Bowman S., Lennard N.J., Doggett J., Ackin R.,  
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,  
Melville S.B., Rajandream M.A. and Barrell B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus,  
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and  
ml@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The V + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects.  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

## FEATURES

LOCATION/Qualifiers  
1..26  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="236d08"

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Best Local Similarity 73.1%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4021 AAGAGAGAGAGAGAGAGAGAG 4046  
DB 1 AAAAAAAAAAAAAAAAAATTTTTT 26

## RESULT 1368

N29432 27 bp mRNA linear EST 05-JAN-1996  
LOCUS N29432  
DEFINITION y86h10.s1 Soares placenta 80c9weeks 2bH8b10c9W Homo sapiens CDNA  
clone IMAGE:259171.3' similar to gp:164559 TERPANEPTIN PRECURSOR  
(HUMAN);, mRNA sequence.  
ACCESSION N29432  
VERSION N29432.1 GI:1147952  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 27)  
Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,  
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,  
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,  
Trevaaskle E., Waterson R., Williamson A., Wohlmann P. and  
Wilson R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

## FEATURES

## source

High quality sequence stops: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Seq primer: m13 -40 forward  
High quality sequence stop: 1.  
Location/Qualifiers

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1. 27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:388877"
/db_xref="taxon:9606"
/clone="IMAGE:259171"
/dev_stage="Two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: placenta; Vector: p773D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo (dt) primer (5'
TGTTACCACTGAGTGGAGCGCGGATTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
```

## Query Match

Best Local Similarity 76.0%; Score 15.4; DB 1; Length 27;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

## Qy

4015 ATGAGAAAAAGAGAGAAAAA 4039

## Db

26 AGGAAAAAAGAAAAA 2

## RESULT 1369

## N52529/c

LOCUS N52529 27 bp mRNA linear EST 15-FEB-1996

DEFINITION YV35a12.g1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone

IMAGE:244702.3 similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN

HIN-1 (HUMAN); mRNA sequence.

ACCESSION N52529

VERSION N52529.1 GI:1193695

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 27)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and

Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: m13 -40 forward

High quality sequence stop: 1.

Location/Qualifiers

```
1. 27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:379398"
/db_xref="taxon:9606"
/clone="IMAGE:244702"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone="11b-Soares fetal liver spleen INFIS"
/notes="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo (dt) primer
(5' AACGGAAGAATTAATTAAGTCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
```

Query Match 0.2%; Score 15.4; DB 1; Length 27;  
Best Local Similarity 73.1%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

## Qy

4009 TCTAAATGAGAAAAAGAGAAAAA 4034

## Db

26 TCNAAAAAAGAAAAA 1

## RESULT 1370

## R37697/c

LOCUS R37697 28 bp mRNA linear EST 04-MAY-1995

DEFINITION YF50C03.g1 Soares infant brain INFIS Homo sapiens cDNA clone

IMAGE:25521.3 similar to gb:U03040 SPARC PRECURSOR (HUMAN); mRNA

sequence.

ACCESSION R37697

VERSION R37697.1 GI:795153

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 28)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and

Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Insert Size: 1410

High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free

through LNL; contact the IMAGE Consortium (info@image.lnl.gov)

for further information. Trace considered overall poor quality

Insert length: 1410 Std Error: 0.00

Seq primer: -21m13

High quality sequence stop: 1.

Location/Qualifiers

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1. 28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:397868"
```

/db\_xref="taxon:9606"  
/clone="IMAGE:25521"  
/sex="female"  
/dev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_id="Soares infant brain INIB"  
/note="Organ: whole brain; Vector: Laifmid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5];  
ACTGAGAGATTGCGGCCGACGAATTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Hind III adaptor (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Laifmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bernaldo."

Query Match 0.2%; Score 15.4; DB 1; Length 28;  
Best Local Similarity 73.1%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4014 AATGAGAAAAAGAGAAACAAA 4039  
Db 28 ACTGAAAAAATAAAAAAANA 3

RESULT 1371  
LOCUS CF299294 28 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-E04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF299294  
VERSION CF299294.1 GI:33671055  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 28)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
location/Qualifiers  
1..28  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--03-E04"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

FEATURES  
source

Query Match 0.2%; Score 15.4; DB 1; Length 28;  
Best Local Similarity 76.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4012 AAAAAAGAGAGAGAAACA 4036  
Db 2 AAAAAAATAAAAAAACA 26

RESULT 1372  
LOCUS BX567540/c 29 bp mRNA linear EST 14-OCT-2003  
DEFINITION BX567540 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse88f02\_p1c, mRNA sequence.  
ACCESSION BX567540  
VERSION BX567540.1 GI:3343463  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 29)  
Lehane,M.J., Ansoy,S., Gibson,W., Kethnou,A., Berriman,M., Hamilton,J., Soares,M.B., Bernaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
MEDLINE 14519198  
PUBMED  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.  
Location/Qualifiers  
1..29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse88f02\_p1c"  
/tissue\_type="adult infected gut"  
/clone\_id="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.Brucei"

Query Match 0.2%; Score 15.4; DB 1; Length 29;  
Best Local Similarity 76.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAACAAATGTTA 4044  
Db 28 AAAAAAATAAAAAAATACTTTA 4

RESULT 1373  
LOCUS CF297930 31 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--01-B17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF297930  
VERSION CF297930.1 GI:33669691  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 31)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. 31

/organism="Oryza sativa"

/mol\_type="mRNA"

/culturivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF-01-B17"

/issue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 31;  
Best Local Similarity 76.0%; Pred. No. 2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 6;

QY 4012 AAAATGAGAAAAAGAGAGAAACA 4036  
Db 7 AAAATGAGAAAAAGAGAGAAACA 31

RESULT 1374  
BF032851 32 bp mRNA linear EST 20-OCT-2000  
LOCUS BF032851 601455689F1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3859127 5',  
DEFINITION mRNA sequence.  
ACCESSION BF032851 GI:10740563  
VERSION BF032851.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 32)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: L1AM9592 row: b column: 24  
High quality sequence stop: 32.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: L1AM9592 row: b column: 24  
High quality sequence stop: 32.

## FEATURES

source

1. 32

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3859127"

/issue\_type="adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_1lb="NIH\_MGC\_66"

/note="Organ: ovary; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

Query Match 0.2%; Score 15.4; DB 1; Length 32;  
Best Local Similarity 76.0%; Pred. No. 2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 6;

QY 4017 GAGAAAAAGAGAGAAACAAATG 4041  
Db 30 GAGAAAAAGAGAGAAACAAATG 6

## RESULT 1375

CF292071/c

LOCUS

DEFINITION

CF292071 34 bp mRNA linear EST 14-AUG-2003  
14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-M02, mRNA sequence.

ACCESSION

CF292071

VERSION

CF292071.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. 34

/organism="Oryza sativa"

/mol\_type="mRNA"

/culturivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ROOT--02-M02"

/issue\_type="root"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 34;  
Best Local Similarity 66.7%; Pred. No. 2e+03; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 11;

QY 3997 AAACTCTTAGCTTAAATGAGAAAAAGAA 4029  
Db 34 AAACTCTTAGCTTAAATGAGAAAAAGAA 2

## RESULT 1376

CF310898/c

LOCUS

DEFINITION

CF310898 35 bp mRNA linear EST 15-AUG-2003  
ABF--05-N05.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-N05, mRNA sequence.

ACCESSION

CF310898

VERSION

CF310898.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 35)



library (HD) *Oryza sativa* cDNA clone HD-07-N06, mRNA sequence.  
 CF317946  
 VERSION CF317946.1 GI:33569707  
 KEYWORDS EST.  
 SOURCE *Oryza sativa*  
 ORGANISM *Oryza sativa*  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; *Oryza*.  
 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..20  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD-07-N06"  
 /issue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 69 GCGGGCGGGCGGCGGCGGCGG 88  
 |||||  
 1 GCGGCGGCGGCGGCGGCGGCGG 20.

RESULT 1380  
 CF319443 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--04-003.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION *Oryza sativa* cDNA clone RCL1--04-003, mRNA sequence.  
 ACCESSION CF319443  
 VERSION CF319443.1 GI:33827271  
 KEYWORDS EST.  
 SOURCE *Oryza sativa*  
 ORGANISM *Oryza sativa*  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; *Oryza*.  
 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..20  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="RCL1--04-003"  
 /issue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site\_1: SacI; Site\_2: XhoI; cDNA was inserted into lambda uni-ZAP XR vector at 5' end with SacI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES  
 source  
 Location/Qualifiers  
 1..20  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="RCL1--04-003"  
 /issue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site\_1: SacI; Site\_2: XhoI; cDNA was inserted into lambda uni-ZAP XR vector at 5' end with SacI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 GCGGCGCAACGAGGCTGC 69  
 |||||  
 1 GCGGCGGCGGCGGCGGCGGCGG 20

RESULT 1381  
 CF340627 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION *Oryza sativa* cDNA clone RCL1--08-K02, mRNA sequence.  
 ACCESSION CF340627  
 VERSION CF340627.1 GI:33829609  
 KEYWORDS EST.  
 SOURCE *Oryza sativa*  
 ORGANISM *Oryza sativa*  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; *Oryza*.  
 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..20  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="RCL1--08-K02"  
 /issue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site\_1: SacI; Site\_2: XhoI; cDNA was inserted into lambda uni-ZAP XR vector at 5' end with SacI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTT 4482  
 |||||  
 Db 1 CTTTTTTTCCCTTTTTTTT 20

RESULT 1382  
 AZ345646 20 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0080K20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 DEFINITION clone UGCGIM0080K20 F, genomic survey sequence.

ACCESSION AZ345646  
 VERSION AZ345646  
 KEYWORDS GI:10424883  
 SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: K column: 20  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4466 TTTTTTTTTTTTTTTGT 4485  
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 Db 20 TTTTTTTTTTAATGTTGT 1

RESULT 1383  
 AZ417235 20 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0192N15R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 DEFINITION clone UGCGIM0192N15 R, genomic survey sequence.

ACCESSION AZ417235  
 VERSION AZ417235.1  
 KEYWORDS GI:10541248  
 SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0192 row: N column: 15  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

#### FEATURES

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 /clone="UGCGIM0192N15"  
 /sex="Male"  
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 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 3635 GAGAGAGCTAGATGGGAA 3654



Db 1 TGCTGCTGCTGCTACTTCC 20  
20 GAGCGGAGGAGAGAGGGA 1

## RESULT 1384

AZ592714

LOCUS

DEFINITION 20 bp DNA linear GSS 13-DEC-2000

clone UGCGIM0403P13 R, genomic survey sequence.

ACCESSION

AZ592714

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

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/organism="Mus musculus"

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.20

/organism="Mus musculus"

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/db\_xref="taxon:10090"

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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

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/organism="Mus musculus"

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Db 1 TGCTGCTGCTGCTACTTCC 20

## RESULT 1385

AZ626475

LOCUS

DEFINITION 20 bp DNA linear GSS 13-DEC-2000

clone UGCGIM0466E16 R, genomic survey sequence.

ACCESSION

AZ626475

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Mus musculus"

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/clone\_1ib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.20

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/db\_xref="taxon:10090"

/clone="UGCGIM0466E16"

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/clone\_1ib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

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/organism="Mus musculus"

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/db\_xref="taxon:10090"

/clone="UGCGIM0466E16"

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.20

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/clone="UGCGIM0466E16"

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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RESULT 1386
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LOCUS      21 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION 1M0282004F Mouse 10kb plasmid U0GCM library Mus musculus genomic
clone U0GCM0282004 F, genomic survey sequence.
ACCESSION  AZ468862
VERSION     AZ468862
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 21)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000      Std Error: 0.00
              Plate: 0282      row: 0      column: 04
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 21.
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                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              Query Match      0.2%; Score 15.2; DB 1; Length 21;
              Best Local Similarity 85.0%; Pred. No. 1.3e+03;
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RESULT 1387
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LOCUS      21 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0465C23F Mouse 10kb plasmid U0GCM library Mus musculus genomic
clone U0GCM0465C23 F, genomic survey sequence.
ACCESSION  AZ625662
VERSION     AZ625662
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 21)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000      Std Error: 0.00
              Plate: 0465      row: 0      column: 04
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 21.
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                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
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                adapted DNA was purified and size-selected for a 9.5 to
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                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              Query Match      0.2%; Score 15.2; DB 1; Length 21;
              Best Local Similarity 85.0%; Pred. No. 1.3e+03;
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RESULT 1388  
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LOCUS TA36B110 21 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. Brucei sheared genomic DNA clone 36ell, reverse sequence,  
genomic survey sequence.  
ACCESSION AL454378  
VERSION AL454378.1 GI:11855182  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
REFERENCE 1 (bases 1 to 21)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
Direct Submision  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhisanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5909 CTGTTCCCAAGCCAGAGA 5928  
DB 20 CTGTTCCACAGTCCAGAGA 1  
|||||  
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RESULT 1389  
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LOCUS A2854229 22 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0157C14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCM0157C14 R, genomic survey sequence.  
ACCESSION A2854229  
VERSION A2854229.1 GI:13043139  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weis, R.  
Niederhausern, A. and Wright, D. Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetice.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0157 row: C column: 14  
Seg primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
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Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5316 TTCTCTCTTTCTCTCTTT 5335  
DB 21 TTTTCTCTTTCTCTCTTT 2  
|||||  
|||||

RESULT 1390  
A2470212  
LOCUS A2470212 22 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0284L09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0284L09 F, genomic survey sequence.  
ACCESSION A2470212  
VERSION A2470212.1 GI:10628337  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weis, R.  
Niederhausern, A. and Wright, D. Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0284 row: L column: 09  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

## Source

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Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U08C1M0284L09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U08C1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4459 TGGACTTTTCTTTTCTTTT 4478  
Db 2 TGGCTTCTTTTCTTTTCTTTT 21

RESULT 1391  
A2875902/c 22 bp DNA linear GSS 21-FEB-2001  
LOCUS  
DEFINITION 2M0190K12R Mouse 10kb plasmid U08C1M library Mus musculus genomic  
ACCESSION A2875902  
VERSION A2875902.1 GI:13086357  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0190 row: K column: 12  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

## Source

1..22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U08C2M0190K12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U08C1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3624 GGTGGGGTGGGAGAGAGAG 3643  
Db 22 GGGGGGGGGGAGAGAGGGG 3

RESULT 1392  
AL587602/c 23 bp mRNA linear EST 02-MAR-2001  
LOCUS  
DEFINITION AL587602 BP Chicken Brain Library Gallus gallus cDNA clone  
ACCESSION R08059F08, mRNA sequence.  
VERSION AL587602  
KEYWORDS EST.

SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus. 1 (bases 1 to 23)  
AUTHORS Murray, F.

JOURNAL BP Chicken Brain Library  
COMMENT Unpublished (2001)  
Contact: Frazer Murray

Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk  
GGGCGCGCTTTTCTTTTCTTTT 3 Poly A RNA purchased from Clontech (\*6854-

FEATURES  
source

Seq primer: M13F.

Location/Qualifiers

1..23  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS059F08"  
/tissue\_type="Brain"  
/dev\_stage="unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3'; 3' adaptor sequence: 5' GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (#6854-1)"

Query Match 0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 81.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4012 AAATGAGAGAGAGAGAA 4032  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAGAGA 3

RESULT 1393  
A2308643

LOCUS A2308643 23 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0011013R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0011013 R, genomic survey sequence.

ACCESSION A2308643  
VERSION A2308643.1 GI:10348845

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0011 row: O column: 13

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

FEATURES  
source

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0011013"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

Query Match 0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4604 TTCTGCCCCACTGCTTGGG 4623  
|||||  
Db 1 TTCTCACCACACTGCTGTG 20

RESULT 1394  
A2345908

LOCUS A2345908 23 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0080F22R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0080F22 R, genomic survey sequence.

ACCESSION A2345908  
VERSION A2345908.1 GI:10425145

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: F column: 22

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

FEATURES  
source

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0080F22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5473 TTTTGTGTAAGATATAT 5492  
Db 22 TTTGTTGTAAGATATATAT 3

RESULT 1395  
LOCUS AZ468097 23 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0279K22R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0279K22 R, genomic survey sequence.

ACCESSION AZ468097  
VERSION AZ468097.1 GI:10626222  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0279 row: K column: 22  
Seq primer: CACACAGAAACACCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

#### FEATURES

source  
1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCLM0279K22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTTGTTGTTT 4483  
Db 4 TTTTGTGTTGTTGTTT 23

RESULT 1396  
LOCUS AZ970753 23 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0244E01F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0244E01 F, genomic survey sequence.

ACCESSION AZ970753  
VERSION AZ970753.1 GI:13841980  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: E column: 01  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

#### FEATURES

source  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCLM0244E01"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.2%; Score 15.2; DB 1; Length 23;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2877 GGAGCTGGGCTAGGAGAG 2896  
3 GGAGCTGGGCTGGGGGCTG 22

RESULT 1397  
A2437459/C  
LOCUS 26 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0225B15R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0225B15 R, genomic survey sequence.  
ACCESSION A2437459  
VERSION A2437459.1 GI:10561472  
KEYWORDS GSS.  
SOURCE Mus musculus  
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 26)  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0225 row: B column: 15  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

#### FEATURES

source  
1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0225B15"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.2%; Score 15.2; DB 1; Length 26;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

4020 AAAAAAGAGAAACAA 4039  
25 AAAAAAGAGAAACAA 6

RESULT 1398  
AM332443/C  
LOCUS 28 bp mRNA linear EST 31-JAN-2000  
DEFINITION S8E7 AGS-1 Pneumocystis carinii CDNA 3', mRNA sequence.  
ACCESSION AM332443  
VERSION AM332443.1 GI:6828800  
KEYWORDS EST.  
SOURCE Pneumocystis carinii  
Pneumocystis carinii  
Pneumocystis carinii  
ORGANISM Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Smallian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,  
Edman, J.C., Kovacs, J. and Cushion, M.  
TITLE Expressed sequence tags from Pneumocystis carinii  
COMMENT Unpublished (2000)  
Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: stabenpop.uky.edu.

FEATURES  
source  
1..28  
Location/Qualifiers

/organism="Pneumocystis carinii"  
/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_1lb="AGS-1"  
/note="Vector: Lambda ZAP II; Site 1: EcoRI, Site 2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Total extracted RNA. Oligo dT priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/Project/Pneumocystis/"

Query Match  
Best Local Similarity 0.2%; Score 15.2; DB 1; Length 28;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

4012 AAAAAAGAGAAACAA 4039  
28 AAAAAAGAGAAACAA 1

RESULT 1399  
TA327D04P/C  
LOCUS 28 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 327D04, forward sequence,  
genomic survey sequence.





Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 15.2; DB 1; Length 29;  
 Best Local Similarity 71.4%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 6964 GAGGAAATGAGCTAATAACCAACGAA 6991  
 1 GAAAGAGAGACCAAAAAAAAAAAAAA 28

RESULT 1402  
 LOCUS CF312595/c 29 bp mRNA linear EST 15-AUG-2003  
 DEFINITION ABF--08-G19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-G19, mRNA sequence.  
 ACCESSION CF312595  
 VERSION CF312595.1 GI:33684356  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4530"  
 /clone="ABF--08-G19"  
 /cissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_id="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15.2; DB 1; Length 29;  
 Best Local Similarity 71.4%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 4015 ATGAGAAAAAGAGGAGAAACAAATGT 4042  
 29 ATAAAAAAAAAAAAAAAAAACTGT 2

RESULT 1403  
 LOCUS TA378G07P/c 29 bp DNA linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 378G07, forward sequence, genomic survey sequence.  
 ACCESSION AL497621  
 VERSION AL497621.1 GI:11873343

KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 29)  
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Omond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrett,B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: [barrett@sanger.ac.uk](mailto:barrett@sanger.ac.uk) and [nh@sanger.ac.uk](mailto:nh@sanger.ac.uk)

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrett, Oxford University Press, 1999).  
 Email: [neilsayed@tigr.org](mailto:neilsayed@tigr.org)  
 Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
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 /clone="378G07"

Query Match 0.2%; Score 15.2; DB 1; Length 29;  
 Best Local Similarity 71.4%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 3271 TTGTGTTAAGAGAAATGAAACCGA 3298  
 29 TTTTAAAAAATAAAAAAAAAAAAAA 2

RESULT 1404  
 LOCUS CF336137/c 29 bp mRNA linear EST 18-AUG-2003  
 DEFINITION JMT--06-B10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-B10, mRNA sequence.  
 ACCESSION CF336137  
 VERSION CF336137.1 GI:33820654  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
 1..29  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"



www.bio.1lnl.gov/bbtp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center <http://www.genome.washington.edu> Low Quality Sequence: 32 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 32 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LICM6 row: G column: 3  
High quality sequence stop: 32.  
Location/Qualifiers  
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/clone="IMAGE:2821274"  
/issue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI, Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally inserted into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match  
Best Local Similarity 0.2%; Score 15.2; DB 1; Length 32;  
Matches 20; Conservativity 71.4%; Pred. No. 2.1e+03;  
Mismatches 8; Indels 0; Gaps 0

QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039  
29 AAAAAAAAAAAAAAAAAATCCAAAAA 2

RESULT 1409  
CF279813/c  
LOCUS  
DEFINITION  
32 bp mRNA linear EST 14-AUG-2003  
14ETL--06-E02.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--06-E02, mRNA sequence.  
ACCESSION  
CF279813  
VERSION  
CF279813.1 GI:33657199  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 32)  
14m.J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6192  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .32  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"

FEATURES  
SOURCE

FEATURES  
SOURCE

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/clone="14ETL--06-E02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_id="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.2%; Score 15.2; DB 1; Length 32;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAAACAAATGTTAT 4045  
 Db 31 AAAAAAAAAAAAAAAAAACCTGCTAT 4

RESULT 1410  
 LOCUS BX558102/c 32 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX558102 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse36f08\_p1c, mRNA sequence.  
 ACCESSION BX558102  
 VERSION BX558102.1 GI:33429249  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kephornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.

## FEATURES

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 /note="country: Zimbabwe; EST from adult gut infected with  
 T.Brucei"

Query Match 0.2%; Score 15.2; DB 1; Length 32;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAAACAAATGTTATTT 4047  
 Db 32 AAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1411  
 LOCUS BX560723/c 32 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX560723 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse50g08\_p1c, mRNA sequence.

ACCESSION BX560723  
 VERSION BX560723.1 GI:33369704  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kephornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.

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 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.Brucei"

Query Match 0.2%; Score 15.2; DB 1; Length 32;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAAACAAATGTTATTT 4047  
 Db 32 AAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1412  
 LOCUS BX564047/c 32 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX564047 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse6d04\_p1c, mRNA sequence.

ACCESSION BX564047  
 VERSION BX564047.1 GI:33431246  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kephornou, A., Berriman, M.,

```

TITLE
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
14519198

JOURNAL
MEDLINE
PUBMED
22881942

COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
Source
Location/Qualifiers
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/clone="Tse6d04_pic"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.2%; Score 15.2; DB 1; Length 32;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy 4020 AAAAAAGAGAAAAACAAATGTTATTT 4047
Db 32 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1413
LOCUS
BX559212/c
DEFINITION
BX559212 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse42c04_pic, mRNA sequence.
ACCESSION
BX559212
VERSION
BX559212.1 GI:33366526
KEYWORDS
EST.
SOURCE
Glossina morsitans morsitans
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae, Glossinidae, Glossina.
1. (bases 1 to 33)
Lehane, M.J., Aksoy, S., Gibson, M., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

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end of the cDNA all pic reads are from
the 3' end.
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/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 15.2; DB 1; Length 33;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy 4020 AAAAAAGAGAGAAACAAATGTTATTT 4047
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Db 32 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1414
BE230585 15 bp mRNA linear EST 07-JUN-2000
LOCUS BE230585/c
DEFINITION 99AS799 Rice Seeding lambda ZAPRI cDNA library Oryza sativa
(indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION BE230585
VERSION BE230585.1 GI:8956782
KEYWORDS EST.
ORGANISM Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Echinozoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
Nahm,B.H.
TITLE large-scale Sequencing Analysis of ESTs from Rice Seeding
JOURNAL Unpublished (1999)
COMMENT Contact: Eun M.Y.
Department of Cyto genetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asi.re.kr.
FEATURES
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XhoI; Directional cDNA library inserted into lambda ZAPRI
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Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTTTTTTTTTTTT 4478
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|||||

Db 15 TTTTTTTTTTTTTT 1

RESULT 1415

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B0582543 15 bp mRNA linear EST 06-DEC-2002  
 LOCUS S013300-024-007-B02-T7 MP12-ADIS-024-inflorance Beta vulgaris  
 DEFINITION cDNA clone 024-007-B02 3-PRIME, mRNA sequence.  
 ACCESSION B0582543  
 VERSION B0582543.1 GI:26112120  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 15 Std Error: 0.00  
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 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinvanzlebener Saatzzucht AG Binbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 Project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1416  
 B0585820 15 bp mRNA linear EST 06-DEC-2002  
 LOCUS E012844-024-014-H17-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
 DEFINITION 024-014-H17 5-PRIME, mRNA sequence.  
 ACCESSION B0585820  
 VERSION B0585820.1 GI:26115402  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
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 cDNA library from sugar beet, library provided by KMS  
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 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 Project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;  
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 ACCESSION B0590410  
 VERSION B0590410.1 GI:26119993  
 KEYWORDS EST.  
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 ORGANISM Beta vulgaris  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189

PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpi-z-koeln.mpg.de  
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 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polys-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;  
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QY 4464 TTTTTTTTTTTTTT 4478  
 Db 1 TTTTTTTTTTTTTT 15

RESULT 1418  
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 LOCUS  
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 ACCESSION CDNA clone 024-018-L13 5-PRIME, mRNA sequence.  
 VERSION BOS90656  
 KEYWORDS BOS90656.1 GI:26120239  
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 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 15)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpi-z-koeln.mpg.de  
 Insert Length: 15 Std Error: 0.00  
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polys-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;  
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 VERSION BOS91170.1 GI:26120753  
 KEYWORDS  
 EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 15)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpi-z-koeln.mpg.de  
 Insert Length: 15 Std Error: 0.00  
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cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatucht AG Bindeck, Germany; contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.2%; Score 15; DB 1; Length 15;
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Db      1  TTTTTTTTTTTTTT 15

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ACCESSION  BO591178
VERSION     BO591178.1 GI:26120761
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ORGANISM    Beta vulgaris
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            1 (bases 1 to 15)
            Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lentrach,H.,
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            22362189
            12472698
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishbaa@mp1z-koeln.mpg.de
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                    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
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                    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
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                    project, local PI: Dr. Katharina Schneider, coordinator:
                    Prof. Christian Jung; Sequence submission managed by
                    RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Prof. Christian Jung: Sequence submission managed by RZPD/GABI-Primary database: <a href="http://gabi.rzpd.de">http://gabi.rzpd.de</a>									
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ACCESSION	BOS91223								
VERSION	BOS91223.1	GI:26120806							
KEYWORDS	EST.								
SOURCE	Beta vulgaris								
ORGANISM	Beta vulgaris								
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.								
AUTHORS	1 (bases 1 to 15) Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lebrach,H. and Radelof,U.								
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes								
JOURNAL	Plant J. 32 (3), 845-857 (2002)								
MEDLINE	12472698								
PUBMED	12472698								
COMMENT	Contact: Weishaar B ADIS DNA core facility at MP1Z Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@mpiz-koeln.mpg.de Insert Length: 15 Std Error: 0.00 Plate: 17 row: H column: 02 Seq primer: T7; GTAATGCACTCACTATAGGC.								
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DB	1	TTTTTTTTTTTTTTTT	15						



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DEFINITION CDNA clone 024-024-M05 3-PRIME, mRNA sequence.  
ACCESSION BOS94689  
VERSION BOS94689.1 GI:26124272  
KEYWORDS EST.  
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ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehmach, H.  
and Radelof, U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
JOURNAL 22362189  
MEDLINE 12472698  
PUBMED  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sall-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-BeeT  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
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Query Match 0.2%; Score 15; DB 1; Length 15;  
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DEFINITION Oryza sativa cDNA clone 14E7L-02-M23, mRNA sequence.  
ACCESSION CF277319  
VERSION CF277319.1 GI:33654705  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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DEFINITION Oryza sativa cDNA clone 14E7L-09-D04, mRNA sequence.  
ACCESSION CF281923  
VERSION CF281923.1 GI:33659310  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TTTT TTTT TTTT TTTT TTTT 15

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ACCESSION  CF290920
VERSION     CF290920.1 GI:33659953
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.
Location/Qualifiers
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1426
LOCUS      CF291029      15 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION  CF291029
VERSION     CF291029.1 GI:33660136
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.
Location/Qualifiers
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ACCESSION  CF291029      15 bp      mRNA      linear      EST 14-AUG-2003
VERSION     CF291029.1 GI:33660062
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
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Oy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1427
LOCUS      CF291103      15 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION  CF291103
VERSION     CF291103.1 GI:33660136
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 1428

LOCUS CF291717 15 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
ACCESSION CF291717  
VERSION CF291717.1 GI:33660750  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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## RESULT 1429

LOCUS CF291798 15 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-G02, mRNA sequence.

ACCESSION CF291798  
VERSION CF291798.1 GI:33660831  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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## RESULT 1430

LOCUS CF292458 15 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
ACCESSION CF292458  
VERSION CF292458.1 GI:33661491  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1431  
 CF292461

LOCUS CF292461 15 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 sativa cDNA clone 30DGS--01-E19, mRNA sequence.

ACCESSION CF292461  
 VERSION CF292461.1 GI:33661494  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongsin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1432  
 CF296652

LOCUS CF296652 15 bp mRNA linear EST 14-AUG-2003

DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 sativa cDNA clone 30DGS--07-C02, mRNA sequence.

ACCESSION CF296652  
 VERSION CF296652.1 GI:33665685  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongsin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1433  
 CF298148

LOCUS CF298148 15 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--01-G17, mRNA sequence.

ACCESSION CF298148  
 VERSION CF298148.1 GI:33669909  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongsin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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1 TTTT TTTT TTTT TTTT 15

RESULT 1434  
CF298630 15 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--02-B23, mRNA sequence.  
ACCESSION CF298630  
VERSION CF298630.1 GI:33670391  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
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RESULT 1435  
CF298733

LOCUS CF298733 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION sativa cDNA clone 7LEAF--02-E20, mRNA sequence.  
CF298733  
VERSION CF298733.1 GI:33670494  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. 15

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1 TTTT TTTT TTTT TTTT 15

RESULT 1436  
CF298805 15 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--02-G20, mRNA sequence.  
ACCESSION CF298805  
VERSION CF298805.1 GI:33670566  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. 15

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with oligoribonucleotides and then used as templates for
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Query Match      0.2%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
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      1 TTTT TTTT TTTT TTTT 15

RESULT 1437
CF298889      15 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION      CF298889
VERSION      CF298889.1 GI:33670650
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT      Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .15
/organism="Oryza sativa"
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/dev stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
      |||||
      1 TTTT TTTT TTTT TTTT 15

RESULT 1438

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CF299602      15 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION      CF299602
VERSION      CF299602.1 GI:33671363
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT      Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .15
/organism="Oryza sativa"
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RT-PCR."

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
      |||||
      1 TTTT TTTT TTTT TTTT 15

RESULT 1439
CF299608      15 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION      CF299608
VERSION      CF299608.1 GI:33671369
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT      Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .15
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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with oligoribonucleotides and then used as templates for
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Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
      |||||
      1 TTTT TTTT TTTT TTTT 15

RESULT 1438

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Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 1440

CF300121

LOCUS CF300121 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF300121  
VERSION CF300121.1 GI:33671882  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT CONTACT: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

1. .15  
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Query Match 0.2%; Score 15; DB 1; Length 15;  
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Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 1441

CF300361

LOCUS CF300361 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF300361  
VERSION CF300361.1 GI:33672122  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT CONTACT: Nahm B.H.

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

1. .15  
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Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 1442

CF300992

LOCUS CF300992 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
ACCESSION CF300992  
VERSION CF300992.1 GI:33672753  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

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/clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
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Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT 15

## RESULT 1443

CEP302034

LOCUS 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CEP302034  
VERSION CEP302034.1 GI:33673795

KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

UNPUBLISHED (2003)

CONTACT: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

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/clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT 15

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT 15

## RESULT 1444

CEP302124

LOCUS 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CEP302124

VERSION CEP302124.1 GI:33673885

KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

UNPUBLISHED (2003)

CONTACT: Nahm B.H.

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

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RT-PCR."
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Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 15

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## RESULT 1445

CEP302182

LOCUS 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CEP302182

VERSION CEP302182.1 GI:33673943

KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

UNPUBLISHED (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.



Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

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/cultivar="Nackdong"

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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1 TTTT TTTT TTTT TTTT 15

Db

## RESULT 1446

CF307923

LOCUS CF307923 15 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--01-115.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-115, mRNA sequence.

ACCESSION CF307923

VERSION CF307923.1 GI:33679684

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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1.15

/organism="Oryza sativa"

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/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--01-115"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
|||||  
1 TTTT TTTT TTTT TTTT 15

Db

## RESULT 1447

CF311159

LOCUS CF311159 15 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.

ACCESSION CF311159

VERSION CF311159.1 GI:33682920

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

CONTACT: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

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/organism="Oryza sativa"

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/cultivar="Nackdong"

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/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

## RESULT 1448

CF311907

LOCUS CF311907 15 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.

ACCESSION CF311907

VERSION CF311907.1 GI:33683668

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
JOURNAL  
COMMENT

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

Location/Qualifiers

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/note="vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
|||||  
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1449  
CF313319

LOCUS HD--01-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION 15 bp mRNA linear EST 15-AUG-2003  
LIBRARY (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313319  
VERSION CF313319.1 GI:33685080  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

Location/Qualifiers

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cDNA library (HD)"

/note="vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
|||||  
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1450  
CF313320/c

LOCUS HD--01-G13.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION 15 bp mRNA linear EST 15-AUG-2003  
LIBRARY (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313320  
VERSION CF313320.1 GI:33685081  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
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Contact: Nahm B.H.  
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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
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/note="vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
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line."

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
|||||  
Db 15 TTTT TTTT TTTT TTTT 1

RESULT 1451  
CF316251/c

LOCUS HD--05-H15.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION 15 bp mRNA linear EST 15-AUG-2003  
LIBRARY (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.

ACCESSION CF316251

VERSION CF316251.1 GI:33688012  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacroidae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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## FEATURES

source

Query Match 0.2%; Score 15; DB 1; Length 15;  
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Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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 Db 15 TTTT TTTT TTTT TTTT 1

RESULT 1452  
 CF318035 15 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD--07-P06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.  
 ACCESSION CF318035  
 VERSION CF318035.1 GI:33689796  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacroidae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1453  
 CF327434 15 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--01-018.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--01-018, mRNA sequence.  
 ACCESSION CF327434  
 VERSION CF327434.1 GI:33803127  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacroidae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligotibonucleotides and then used as templates for RT-PCR."

## FEATURES

source

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
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Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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 Db 1 TTTT TTTT TTTT TTTT 15

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RESULT 1454
CF330195      15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION   NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION    CF330195
VERSION      CF330195.1  GI:33808618
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euhartioideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.2%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1455
CF330668      15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION   NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION    CF330668
VERSION      CF330668.1  GI:33809572
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euhartioideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193

```

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
SOURCE
1..15
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1456
CF332178      15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION   NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION    CF332178
VERSION      CF332178.1  GI:33812580
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euhartioideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 1457  
CF336202  
LOCUS  
DEFINITION CF336202 15 bp mRNA linear EST 18-AUG-2003  
JMT--06-C20.b1 AtUMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.  
ACCESSION CF336202  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
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/organism="Oryza sativa"  
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478  
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1 TTTT TTTT TTTT TTTT 15

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1458  
BOS90507  
LOCUS  
DEFINITION BOS90507 16 bp mRNA linear EST 06-DEC-2002  
E01844-024-019-M04-T7 MP12-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-019-M04 3-PRIME, mRNA sequence.  
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VERSION  
KEYWORDS  
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ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 16)  
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189  
PUBMED 12472698  
COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@piz-koeln.mpg.de  
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/note="Vector: PCWVS-PORT6, Site\_1: SalI; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 TTTT TTTT TTTT TTTT 15

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S01317-024-022-P02-T7 MP12-ADIS-024-developing root Beta vulgaris  
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ACCESSION BOS95369  
VERSION  
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SOURCE EST.  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 16)  
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@piz-koeln.mpg.de  
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 SP6-SalI-CCACGCGTCG-5prime-cDNA-PolyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 16;  
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1460  
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LOCUS CP3296130 16 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza  
 sativa cDNA clone 30DGS--06-F22, mRNA sequence.

ACCESSION CP3296130  
 VERSION CP3296130.1 GI:33665163  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eubharitoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE Oryza sativa  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnah@gbio.com, bhnahmbio.myongji.ac.kr.

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1461

LOCUS CP314013 16 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD-02-G01.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa cDNA clone HD-02-G01, mRNA sequence.

ACCESSION CP314013  
 VERSION CP314013.1 GI:33685774  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eubharitoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE Oryza sativa  
 JOURNAL Contact: Nahm B.H.  
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnah@gbio.com, bhnahmbio.myongji.ac.kr.

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Query Match 0.2%; Score 15; DB 1; Length 16;  
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1462

LOCUS CP329320 16 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL-04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL-04-J17, mRNA sequence.

ACCESSION CP329320  
 VERSION CP329320.1 GI:33806877  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 line."

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1462

LOCUS CP329320 16 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL-04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL-04-J17, mRNA sequence.

ACCESSION CP329320  
 VERSION CP329320.1 GI:33806877  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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## RESULT 1463

CF311499

LOCUS CF311499 17 bp mRNA linear EST 15-AUG-2003  
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 library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.

ACCESSION

CF311499  
 VERSION CF311499.1 GI:33683260

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 location/Qualifiers  
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cDNA library (ABF)"  
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 then used for PCR. mRNA was prepared from ABA-responsive  
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 line."

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## RESULT 1464

CF298591

LOCUS CF298591 18 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION

CF298591  
 VERSION CF298591.1 GI:33670352

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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## RESULT 1465

CF301359

LOCUS CF301359 18 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION

CF301359  
 VERSION CF301359.1 GI:33673120

KEYWORDS

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SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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          1 TTTT TTTT TTTT TTTT 15

Db      1 TTTT TTTT TTTT TTTT 15

RESULT 1466
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LOCUS      ABF--03-119.b1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION   CF309376
VERSION     CF309376.1 GI:33681137
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Db      1 TTTT TTTT TTTT TTTT 15

RESULT 1467
CF329484      18 bp mRNA linear EST 18-AUG-2003
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            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329484
VERSION     CF329484.1 GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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RESULT 1468
CF329485/c      18 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329485
VERSION     CF329485.1 GI:33807208
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1..18
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="NACL--04-N06"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

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active cDNA clone NACL-04-N06, mRNA sequence.

CF329485  
VERSION  
CF329485.1 GI:33807209

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

FEATURES  
source  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

1. 18  
/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL-04-N06"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred.No.1e+03; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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RESULT 1469

CF278272 19 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ETL-04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

DEFINITION Oryza sativa cDNA clone 14ETL-04-C01, mRNA sequence.

ACCESSION CF278272.1 GI:33655658

VERSION  
KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

FEATURES  
source  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

1. 19  
/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL-04-N06"

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/db\_xref="taxon:4530"

/clone="14ETL-04-C01"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No.1.1e+03; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
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RESULT 1470

CF308042 19 bp mRNA linear EST 15-AUG-2003  
LOCUS ABR--01-L07.b1 ABR3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABR--01-L07, mRNA sequence.

DEFINITION ABR--01-L07.b1 ABR3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABR--01-L07, mRNA sequence.

ACCESSION CF308042

VERSION  
KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

FEATURES  
source  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

1. 19  
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/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--01-L07"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABR-responsible element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No.1.1e+03; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 1471
AZ465954
LOCUS 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0276E18F Mouse 10kb plasmid U0GCLM library Mus musculus genomic
clone U0GCLM0276E16 F, genomic survey sequence.
ACCESSION
AZ465954
VERSION
AZ465954.1 GI:10624079
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduan@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 Row: B Column: 16
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="U0GCLM0276E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U0GCLM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid p1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4463 CTTTTTTTTTTTTT 4477
DB 5 CTTTTTTTTTTTTT 19

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RESULT 1472
CF282165
LOCUS 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL-09-122.G1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL-09-122, mRNA sequence.
ACCESSION
CF282165
VERSION
CF282165.1 GI:33659552
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Oryzoae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL-09-122"
/risue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1; EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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FEATURES
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/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="14ETL-09-122"
/risue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1; EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TTTTTTTTTTTTTG 15

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RESULT 1473
AZ596349
LOCUS 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0409K03R Mouse 10kb plasmid U0GCLM library Mus musculus genomic
clone U0GCLM0409K03 R, genomic survey sequence.
ACCESSION
AZ596349
VERSION
AZ596349.1 GI:11718539
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0409 row: K column: 03  
Seq primer: CACACGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

## FEATURES

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0409K03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3616 GGGATGGGCTGGCG 3630  
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Db 7 GGGATGGGCTGGCG 21

RESULT 1474  
A2375417/c 22 bp DNA linear GSS 02-OCT-2000  
LOCUS A2375417  
DEFINITION IM0128B13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0128B13 R, genomic survey sequence.  
ACCESSION A2375417  
VERSION A2375417.1 GI:10489117  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0128 row: E column: 13  
Seq primer: CACACGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTT 4477  
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Db 21 CTTTCTTTTCTTTT 7

RESULT 1475  
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LOCUS A2425710  
DEFINITION IM0205123R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0205123 R, genomic survey sequence.  
ACCESSION A2425710  
VERSION A2425710.1 GI:10549723  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0205 row: L column: 23  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers

## FEATURES

SOURCE

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 /organism="Mus musculus"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAA 4039  
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 Db 1 GAAAAA 23

RESULT 1476  
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 LOCUS AZ621676  
 DEFINITION IM0455J07F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 clone UGGCM0455J07 F, genomic survey sequence.  
 ACCESSION AZ621676  
 VERSION AZ621676.1 GI:11743962  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0455 row: J column: 07  
 Seq primer: CATTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers

## FEATURES

SOURCE

1..23  
 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAAAA 4042  
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 Db 1 AAAAAA 23

RESULT 1477  
 AZ817623 23 bp DNA linear GSS 20-FEB-2001  
 LOCUS AZ817623  
 DEFINITION 2M0687N09F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 clone UGGCM0087N09 F, genomic survey sequence.  
 ACCESSION AZ817623  
 VERSION AZ817623.1 GI:12987531  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177



Db	1	TTTTTTTCTTAATAATA 23
RESULT 1480		
LOCUS	CB305256	
DEFINITION	3'EST-NTfy-071 Drosophila melanogaster cDNA Library Drosophila	23 bp mRNA linear EST 01-JUN-2003
ACCESSION	CB305256	
VERSION	CB305256.1	GI:31297660
KEYWORDS	EST.	
SOURCE	Drosophila melanogaster (fruit fly)	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 23)	
AUTHORS	Lee,S., Zhou,G., Bao,J., Shapiro,J., Xu,J., Sun,M., Lin,W., Zhang,R., Chen,D., Clark,T., Sun,M., Wang,Y., Johnson,D., Tseng,C., Yang,H., Wang,J., Du,W., Wu,C.I., Zhang,X. and Wang,S.M.	
TITLE	Novel SAGE tags represent a significant number of novel genes in Drosophila genome	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Wang SM Hem/Onc University of Chicago Medical Center 5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA Tel: 773-702-6788 Fax: 773-702-3002 Email: swangj@midway.uchicago.edu This EST was detected from Drosophila melanogaster cDNA library with GIGI technique (Generation of Longer cDNA fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000). A high-throughput GIGI procedure for converting a large number of SAGE tag sequences into 3' ESTs Genes, Chromosomes & Cancers 33:252-261, 2002 ), which covers from the 3' end of cDNA till the first CATG. Seq primer: M13 Forward. Location/Qualifiers 1..23 /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /clone_lib="Drosophila melanogaster cDNA library"	
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Query Match	0.2% Score 15; DB 1; Length 23;	
Best Local Similarity	78.3%; Pred. No. 1.6e+03;	
Matches	18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Oy	4474 TTTTTCCTTGAGACATG 4496	
Db	1 TTTTTCCTTGAGACATG 23	
RESULT 1481		
LOCUS	AZ303987/c	
DEFINITION	1M0003H22R Mouse 10kb plamid tUCGIM library Mus musculus genomic clone UCGIM0003H22 R, genomic survey sequence.	23 bp DNA linear GSS 29-SEP-2000
ACCESSION	AZ303987	
VERSION	AZ303987.1	GI:10339507
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)	
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.	
AUTHORS	Niederhausern,A. and Wright,D.,Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

JOURNAL

COMMENT

Plasmid insects  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: H column: 22  
Seq primer: CACGACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

FEATURES

source

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M003H22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb|AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 7097 GTACCAATTAAGAAA 7111  
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DB 15 GTACCAATTAAGAAA 1

RESULT 1482

AZ380872 23 bp DNA linear GSS 02-OCT-2000  
LOCUS 1M0137H02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0137H02 F, genomic survey sequence.  
ACCESSION AZ380872 GI:10494572  
VERSION AZ380872.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid insects

JOURNAL Unpublished (2000)  
COMMENT Contract: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0137 row: H column: 02  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

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Source  
1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0137H02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCM1 library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 (gi14732114[gb|AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Cy 4027 AGAGAAACCAATGTTATTTT 4049  
Db 1 AAAAAAAAAAATTTTTTTTTT 23

RESULT 1483  
AZ398873/c 23 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0164P21F Mouse 10kb plasmid UGCM1 library Mus musculus genomic  
DEFINITION clone UGCM1M0164P21 F, genomic survey sequence.  
ACCESSION AZ398873  
VERSION AZ398873.1 GI:10513945  
KEYWORDS GSS.  
ORGANISM Mus musculus (house mouse)  
SOURCE Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Jellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
Niederhauser,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

COMMENT	FEATURES	source
<p>Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: rdunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0164 row: P column: 21 Seq primer: CGTTGTTAAACGACGGCCAGT Class: plasmid end High quality sequence stop: 23.</p>	<p>Location/Qualifiers 1. 23 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGGCM0164P21" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_1b="Mouse 10kb plasmid UGGCM library" /note="Vector: PMD29ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."</p>	<p>Query Match Best Local Similarity 78.3%; Pred. No. 1.6e+03; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 3621 TGGGCTGGGGCTGGGAGAGGAGG 3643 Db 23 TGGGGGGGGGGGGGGGGGGGGGGG 1  <div> <div>     </div> <div>     </div> </div> </p>
<p>RESULT 1484 A2439451/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS ORGANISM SOURCE REFERENCE AUTHORS TITLE JOURNAL COMMENT</p>	<p>23 bp DNA 1linear GSS 03-OCT-2000 IM0230C09F Mouse 10kb plasmid UGGCM library Mus musculus genomic clone UGGCM0230C09 F, genomic survey sequence. A2439451 A2439451.1 GI:10563464 GSS. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss</p>	

University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0230 row: C column: 09  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.

## FEATURES

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0230C09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gl14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 1.e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3622 GCGGTGGGGTGGAGAGAGGT 3644  
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 Db 23 GGGGGGGGGGGGGGGGGGGGT 1

## RESULT 1485

AZ632757 23 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0487M05R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0487M05 R, genomic survey sequence.

ACCESSION AZ632757  
 VERSION AZ632757.1 GI:11754947  
 GSS.

KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiser, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## TITLE

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0487 row: M column: 05  
 Seq primer: CACACAGAAACAGCATATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.

## FEATURES

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gl14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 1.e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4461 GACTTTTCTTTTCTTTTCTTTT 4483  
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 Db 1 GTCTCTTTTCTCTTTTGT 23

## RESULT 1486

TA229C120 23 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 229C12, reverse sequence,  
 genomic survey sequence.

ACCESSION AL480862  
 VERSION AL480862.1 GI:11846631  
 GSS.

KEYWORDS Trypanosoma brucei  
 SOURCE Trypanosoma brucei

## ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

1 (bases 1 to 23)

## REFERENCE

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.B., Rajandream, M.A. and Barrell, B.G.  
 Direct Submision  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

## TITLE

JOURNAL

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of



Trypanosoma brucei (TR927/4 GUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaundin and B. Barrell, Oxford University Press, 1999).

Email: nelyaved@icr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

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/clone="229c12"

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 1.6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4455 GGCATGACTTTTCTTTTCTTTT 4477

Db 1 GCGCGGCGGCTTTTCTTTTCTTTT 23

## RESULT 1487

A2812579

LOCUS A2812579 24 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0079A23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0079A23 F, genomic survey sequence.

ACCESSION A2812579  
VERSION A2812579.1 GI:12981965

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std. Error: 0.00  
Plate: 0078 Row: A Column: 23  
Seq primer: CGTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

## FEATURES

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/strain="C57BL/6J"  
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/lab\_host="B. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
<http://www.jax.org/resources/documents/dnares/>. The DNA

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 1.7e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAGAAAA 4039

Db 2 GAAAAAAGAAAAA 24

## RESULT 1488

A2438069

LOCUS A2438069 24 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0228A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0228A10 F, genomic survey sequence.

ACCESSION A2438069  
VERSION A2438069.1 GI:10562178

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std. Error: 0.00  
Plate: 0228 Row: A Column: 10  
Seq primer: CGTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

## FEATURES

source

1. 24  
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/mol\_type="genomic DNA"  
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/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
<http://www.jax.org/resources/documents/dnares/>. The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAGAGAGAAACAAAT 4040  
Db 1 AAAAAAAAAAAAAAAAAATTTT 23

## RESULT 1489

A2764496

LOCUS 24 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0560H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560H02 R, genomic survey sequence.  
ACCESSION A2764496  
VERSION A2764496.1 GI:12879519

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb

## TITLE

plasmid inserts

## JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0560 row: H column: 02  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

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/note="Vector: pMD2nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4021 AAGAGAGAGAAACAAATGTT 4043  
Db 1 AAAAAAAAAAAAAAAAAATTTT 23

## RESULT 1490

A2764513

LOCUS 24 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0560D11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560D11 R, genomic survey sequence.  
ACCESSION A2764513  
VERSION A2764513.1 GI:12879553

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
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## TITLE

plasmid inserts

## JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0560 row: D column: 11  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

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/note="Vector: pMD2nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4021 AAAAGAGAGAAACAAATGTT 4043  
Db 1 AAAAAAAAAAAAAAAAAATTTT 23

RESULT 1491  
A2448207 24 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0245E16R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
DEFINITION clone UGCLM0245E16 R, genomic survey sequence.

ACCESSION A2448207  
VERSION A2448207.1 GI:10600777  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, B., Haml, C.,  
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3271 TTGTGTTAGAGAAATGATAA 3293  
Db 1 TTTTAAAAAAAAAAAAAAAAA 23

RESULT 1492  
AL048782 25 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZP566O013\_r1 566 (synonym: hfk42) Homo sapiens cDNA clone  
DEFINITION DKFZP566O013, mRNA sequence.

ACCESSION AL048782  
VERSION AL048782.1 GI:4727853  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 25)  
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Koehler, et al.)  
Unpublished (1999)  
JOURNAL Contact: MIPS  
COMMENT MIPS

TITLE Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS

FEATURES  
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/clone\_1lb="566 (synonym: hfk42)"  
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Location/Qualifiers

QY 4017 GAGAAAAAGAGAGAAACAAA 4039  
Db 2 GAGACAAAAAAAAAAAAAAAAA 24

RESULT 1493  
CF301712/c 25 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--06-K21, mRNA sequence.

ACCESSION CF301712  
VERSION CF301712.1 GI:33673473  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 DB 25 GAAAAAAAAAAAAAAAAAAAAA 3

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 LOCUS 2M0113M21F Mouse 10kb plasmid UUGCM library Mus musculus genomic  
 DEFINITION clone UUGCM0113M21 F, genomic survey sequence.  
 ACCESSION AZ832800  
 VERSION AZ832800.1 GI:13002708  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 JOURNAL plasmid inserts  
 COMMENT Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 Seq primer: GGTGTAAACGACGCGCAGT  
 CLASS: plasmid ends  
 High quality sequence stop: 25.  
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/organism="Mus musculus"  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMP42 (GI4732114|DB|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 25;  
 Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 4017 GAGAAAAAGAGAAAAACAAA 4039  
 DB 24 GAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1495  
 AL587648/c 25 bp mRNA linear EST 02-MAR-2001  
 LOCUS AL587648 BP Chicken Brain library Gallus gallus cDNA clone  
 DEFINITION ROS060C07, mRNA sequence.  
 ACCESSION AL587648  
 VERSION AL587648.1 GI:13192682  
 KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Murray,F  
 TITLE BP Chicken Brain library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Frazer Murray  
 Dept. Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UK  
 Tel: +44 (0)131 527 4200  
 Fax: +44 (0)131 440 0434  
 Email: frazer.murray@bsrc.ac.uk  
 GGGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech  
 (+6854-

FEATURES  
 source location/Qualifiers  
 1..25

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Query Match 0.2%; Score 15; DB 1; Length 25;  
 Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
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QY 4018 AAAAAAAAAAGAGAGAAAAAATAAT 4040  
 Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 1496  
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 DEFINITION clone UGCGIM0137N18 F, genomic survey sequence.  
 ACCESSION AZ381039  
 VERSION AZ381039.1 GI:10494739  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 Plate: 0137 row: N column: 18  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 25.

FEATURES  
 source Location/Qualifiers

1..25  
 /organism="Mus musculus"  
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 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone.lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 ligated to the blunt ends in high molar excess. The  
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 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 25;  
 Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4018 AAAAAAAAAAGAGAGAAAAAATAAT 4040  
 Db 3 AAAAAAAAAAAAAAAAAAAAAAAAAAT 25

RESULT 1497  
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 DEFINITION clone UGCGIM0146A08 F, genomic survey sequence.  
 ACCESSION AZ386891  
 VERSION AZ386891.1 GI:10500591  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 High quality sequence stop: 25.

FEATURES  
 source Location/Qualifiers

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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGAAACAAAT 4040  
Db 2 AAAAAAAAAAAAAAAAAAAT 24

## RESULT 1498

LOCUS AU265663/c

DEFINITION AU265663 VS Dictyostelium discoideum cDNA clone VSF713 5', mRNA sequence.

ACCESSION AU265663

VERSION AU265663.1 GI:20524461

KEYWORDS EST.

SOURCE Dictyostelium discoideum

ORGANISM Dictyostelium discoideum

REFERENCE 1 (bases 1 to 25)

Unruhshara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,

Takeuchi, I., Kohara, Y., and Tanaka, Y.

Population analysis of cDNAs from unicellular and multicellular

stages of Dictyostelium discoideum

Unpublished (2002)

CONTACT: Hideko Unruhshara

Institute of Biological Sciences

University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-4664

Fax: 81-298-53-6614

Email: hideko@biol.tsukuba.ac.jp.

## FEATURES

source

1..25  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSF713"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_11b="VS"

Query Match 0.2%; Score 15; DB 1; Length 25;

Best Local Similarity 78.3%; Pred. No. 1.8e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGAAACAAAT 4040  
Db 23 AAAAAAAAAAAAAAAAAAAT 1

## RESULT 1499

LOCUS T49097/c

DEFINITION T49097 25 bp mRNA linear EST 06-FEB-1995  
ybo08h08.s1 StrataGene placenta (#937225) Homo sapiens cDNA clone  
IMAGE:706233; similar to similar to gb:K62744 CLASS II  
HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097

VERSION T49097.1 GI:650957

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 25)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, N.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Madsen, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,  
and Warr, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL MEDLINE PUBMED

Other ESTs: ybo08h08.r1

Contact: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21ml3

High quality sequence stop: 1.

## FEATURES

source

1..25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:491520"  
/db\_xref="taxon:9606"  
/clone="IMAGE:70623"  
/sex="male"  
/lab\_host="SOLR cells (Kanamycin resistant)"  
/clone\_11b="Stratagene placenta (#937225)"  
/note="Organ: placenta; Vector: pBlueScript SK-; Site: 1:  
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
XR Vector; -5' adaptor sequence: 5' GAATTCGACACAG 3' -3'  
adaptor sequence: 5' CTCGATTTTCTTTTCTTTTCTTTT 3'"

Query Match 0.2%; Score 15; DB 1; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3271 TTGCTTAAGAGAAATGAA 3293  
Db 25 TTCTTAAAAAAAAAAAAA 3

## RESULT 1500

LOCUS TA12P02Q

DEFINITION TA12P02Q 25 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 12102, reverse sequence.  
genomic survey sequence.

ACCESSION AL451366

VERSION AL451366.1 GI:11833388

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 25)

Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1. .25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="12f02"

## Query Match

Best Local Similarity 0.24; Score 15; DB 1; Length 25;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

## QY

3271 TTGTGTTAAGACGAAATGAAA 3293  
2 TTTTGTAAAAAATGAAAAA 24

## Db

## RESULT 1501

AL587774/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

26 bp mRNA linear EST 02-MAR-2001  
AL587774 BP Chicken Brain Library Gallus gallus cDNA clone  
AL587774 mRNA sequence.  
AL587774.1 GI:13192808  
EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianidae; Gallus.  
1 (bases 1 to 26)  
Murray, F.  
BP Chicken Brain Library  
Unpublished (2001)  
Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@berc.ac.uk  
GCGGCGGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech  
(\*6854-  
Seq primer: M13F.

## FEATURES

source

Location/Qualifiers  
1. .26  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS063A11"  
/issue\_type="Brain"  
/dev\_stage="unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned  
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:  
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'  
GGGCGGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from  
Clontech (\*6854-1)"

Query Match 0.24; Score 15; DB 1; Length 26;  
Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4018 ACAAAGAGAGAGAGAGAGAGAT 4040  
23 AAAAAAAAAAAAAAAAAAAAAAT 1

## RESULT 1502

AZ862643/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

27 bp DNA linear GSS 21-FEB-2001  
AZ862643  
2M0170J19F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCGM0170J19 F, genomic survey sequence.  
AZ862643.1 GI:13060151  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0170 row: J column: 19  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0170J19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and 14  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

source

Location/Qualifiers  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0170J19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and 14  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.24; Score 15; DB 1; Length 27;  
Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;





Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

1. 27  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cullivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF-06-B07"  
/feature\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABP)"  
/note="vector: pCR4-TOPO, Site\_1, EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 27;  
Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5407 CATTCAAGAAATTAAGACAGA 5429  
DB 23 CATTCAAAAAAAAAAAAAAAAA 1

## RESULT 1506

AZ495352/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

27 bp DNA linear GSS 05-OCT-2000  
1M0331E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0331E14 F, genomic survey sequence.  
AZ495352  
AZ495352.1 GI:10670743  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0331 row: E column: 14  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1. 27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0331E14"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnars/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 27;  
Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAGAAA 4034  
DB 23 AAAAGAGAAAAAGAGAGAAA 1

## RESULT 1507

AZ953355/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

27 bp DNA linear GSS 27-APR-2001  
2M0218M01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0218M01 R, genomic survey sequence.  
AZ953355  
AZ953355.1 GI:13824582  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0218 row: M column: 01  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1. 27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0218M01"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson

Query Match	0.2%;	Score 15;	DB 1;	Length 28;
Best Local Similarity	72.0%;	Pred. No. 2e+03;		
Matches 18;	Conservative . 0;	Mismatches 7;	Indels 0;	Gaps 0;

1' strand cDNA was primed with a Pac I - oligo(dT) primer  
15' AACTGGAGAGATTATTAAGATCTTTTTTTTTTTTTTTT 3',  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bente Soares and M.Fátima Bonaldó."

RESULT 1510			
AL048741			
LOCUS	29 bp	mRNA	linear
AL048741			EST 04-SEP-2003

```

DEFINITION   DKF2566J063.r1.566 (synonym: hfk2) Homo sapiens cDNA clone
ACCESSION    AL048741
VERSION      AL048741.1 GI:4727812
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 29)
AUTHORS      Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE        EST (Koehrer, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS         Ingolstedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES     source
             1..29
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="DKF2566J063"
             /issue_type="Kidney"
             /dev_stage="fetal"
             /lab_host="X1-2blue"
             /clone_1ib="566 (synonym: hfk2)"
             /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.2%; Score 15; DB 1; Length 29;
Best Local Similarity 78.3%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
      ||||| ||||| ||||| |||||
      7 GGGAAAAAAGAAAAAAGAAAAA 29

RESULT 1511
LOCUS       AU267990 29 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267990 VS Dictyostelium discoideum cDNA clone VSH801 5', mRNA
sequence.
ACCESSION   AU267990
VERSION     AU267990.1 GI:20526788
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
ORGANISM    Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 29)
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobiol.tsukuba.ac.jp.
FEATURES     source
             1..29
             /organism="Dictyostelium discoideum"
             /mol_type="mRNA"
             /strain="AX4"
             /db_xref="taxon:44689"
             /clone="VSH801"
             /sex="mat A"
             /dev_stage="vegetative"
             /clone_1ib="VS"

Query Match      0.2%; Score 15; DB 1; Length 29;

```

```

Best Local Similarity 78.3%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4011 TAAATGAGAAAAAGAGAAA 4033
      ||||| ||||| ||||| |||||
      28 TAAAAAAGAAAAAAGAAAAA 6

RESULT 1512
LOCUS       TA244G08P/C 31 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 244G08, forward sequence,
genomic survey sequence.
ACCESSION   AL483539
VERSION     AL483539.1 GI:11849040
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
ORGANISM    Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 31)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhls@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..31
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="244G08"

FEATURES     source
             1..31
             /organism="Trypanosoma brucei"
             /mol_type="genomic DNA"
             /strain="TREU927"
             /db_xref="taxon:5691"
             /clone="244G08"

Query Match      0.2%; Score 15; DB 1; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
      ||||| ||||| ||||| |||||
      28 GGGAAAAAAGAAAAAAGAAAAA 6

RESULT 1513
LOCUS       AL588429 32 bp mRNA linear EST 02-MAR-2001
DEFINITION AL588429 BP Chicken Brain Library Gallus gallus cDNA clone
sequence.
ACCESSION   AL588429
VERSION     AL588429.1 GI:13193463
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
1 (bases 1 to 32)
Murray,F.

Query Match      0.2%; Score 15; DB 1; Length 29;

```

TITLE BP Chicken Brain Library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk  
GCGCCGCTTTTCTTTTCTTTTCTT 3' Poly A RNA purchased from Clontech  
(\*6854-

FEATURES  
source

Seq primer: T7.  
Location/Qualifiers  
1..32  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS072C03"  
/tissue\_type="Brain"  
/dev\_stage="Unknown"  
/lab\_host="MDH10B"  
/clone\_lib="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; Cloned  
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:  
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'  
GCGCCGCTTTTCTTTTCTTTTCTT 3' Poly A RNA purchased from  
Clontech (\*6854-1)"

Query Match 0.2%; Score 15; DB 1; Length 32;  
Best Local Similarity 78.3%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 4018 AGAAAAAGAGAAACAAAT 4040  
Db 31 AAAAAAAAAAAAAAAAAAAT 9

## RESULT 1514

AZ869514

LOCUS 32 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0181107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0181107 R, genomic survey sequence.

ACCESSION

AZ869514

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 32)  
Dunn, P., Acovagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

JOURNAL

COMMENT

PUBMED

UNPUBLISHED

CONTACT

UNIVERSITY

OF

UTAH

GENOME

CENTER

RM.

308,

BIOMEDICAL

POLYMERS

RESEARCH

Bldg.,

20 S.

2030 E.,

SLC,

UT

84112, USA

TEL:

801 585 5606

FAX:

801 585 7177

EMAIL:

ddunn@genetics.utah.edu

INSERT

LENGTH:

10000

STD

ERROR:

0.00

PLATE:

0181

ROW:

I

COLUMN:

07

SEQ

PRIMER:

CACACGAGAAACAGCTAGACC

CLASS:

plasmid ends

High

quality

sequence

stop:

32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0181107"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD22ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 32;  
Best Local Similarity 67.7%; Pred. No. 2.1e+03;  
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Cy 4008 GTCTAAATGAGAAAAAGAGAAACANA 4038  
Db 1 GTCTGAAAAACCAAAAAAAAAAAAAA 31

## RESULT 1515

BX555533/c

LOCUS 32 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX555533 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse21c01\_p1c, mRNA sequence.

ACCESSION

BX555533

VERSION

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.

REFERENCE

AUTHORS

1 (bases 1 to 32)  
Lehane, M.J., Akroy, S., Gibson, W., Kethornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE

JOURNAL

COMMENT

PUBMED

UNPUBLISHED

CONTACT

HALL

N

PATHOGEN

SEQUENCING

UNIT

THE

WELLCOME

TRUST

GENOME

CAMPUS

SANGER

INSTITUTE,

CAMBRIDGE,

CB10 1SA, UK

REQUEST

FOR

CLONES,

PLEASE

CONTACT:

MIKE

LEHANE

SCHOOL

OF

BIOLOGICAL

SCIENCES,

UNIVERSITY

OF

WALES,

BANGOR

LL57 2UW

ALL

clones

with

suffix

pic

are

reverse

primer

reads

starting

at

5'

end

of

the

cDNA

all

pic

reads

are

from

the

3' end.

Location/Qualifiers

1..32

/organism="Glossina morsitans morsitans"

```

/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse21c01_p1c"
/cisue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 15; DB 1; Length 32;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
|||||
32 GAGCAAAAAAAAAAAAAAAAAAAAA 10

RESULT 1516
BX564081/c 33 bp mRNA linear EST 10-OCT-2003
LOCUS BX564081 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse6f01_p1c, mRNA sequence.
ACCESSION BX564081
VERSION BX564081.1 GI:33431278
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 33)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Journal Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES
source 1..33
Location/Qualifiers
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse6f01_p1c"
/cisue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 15; DB 1; Length 33;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
|||||
33 GACCAAAAAAAAAAAAAAAAAAAAA 11
DB

```

```

RESULT 1517
AM246505 18 bp mRNA linear EST 07-JAN-2000
LOCUS AM246505
DEFINITION 2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
mRNA sequence.
ACCESSION AM246505
VERSION AM246505.1 GI:6589498
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 18)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821585.5prime
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/btrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu low Quality Sequence: 18
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 18 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LCM7 row: D column: 2
High quality sequence stop: 18.
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821585"
/cisue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTCTTTT 4481
|||||
1 TTTTTCCTTTTCTTTT 18
DB

RESULT 1518
CF329020 18 bp mRNA linear EST 18-AUG-2003
LOCUS CF329020
DEFINITION NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence.

```

ACCESSION CF329020 GI:33806277  
VERSION CF329020.1  
KEYWORDS EST.  
SOURCE  
ORGANISM Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim,Y.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

JOURNAL COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myoungil University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongil.ac.kr.

FEATURES  
Source Location/Qualifiers  
1..18  
/organism="Oryza sativa"  
/mol\_type="RNA"  
/culivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL-04-D03"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2n6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPo; Site 1: EcoRI; mRNA was capped  
with oligobionucleotides and then used as templates for  
RT-PCR."

Query Match 0.2% Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred.No.1.le+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 4469 TTTTTCCTTTTTTTGTC 4486  
|||||  
Db 1 TTTTTCCTTTTTTACTC 18

RESULT 1519  
A1371092 LOCUS A1371092 19 bp mRNA linear EST 16-FEB-1999  
DEFINITION ta07g09.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2043424 3'  
similar to TR:Q26195 Q26195 PVAI GENE; contains 11.b3 LI  
repetitive element ; , mRNA sequence.  
A1371092  
A1371092.1 GI:419845  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 19)  
NCJ/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGA), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: rgsapbe@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonafide, Ph.D.  
DNA Sequenced by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E.B. Consortium/LIML at:

```

www-bio.1ln1.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 536      Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers

1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/clone_1lb="NCI_CGAP_Brn23"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTGATGAGGAGGCGGACATCTTTTCTTTTCTTTTCTTTT
T 3'], double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

Query Match      0.2%; Score 14.8; DB_1; Length 19;
Beet Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5709 TTTTCTCTCTCTCTCTT 5726
1 TTTTCTTTTCTCTT 18

RESULT 1520
CE309858/c
LOCUS
DEFINITION
ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
11braty (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.
ACCESSION
CE309858
VERSION
CE309858.1 GI:33681619
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
SOURCE
1. 19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-D16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI, Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and

```



REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomyces.

AUTHORS 1 (bases 1 to 20)  
TITLE Morimyo,M. and Mita,K.  
Identification of expressed sequence tags of Schizosaccharomyces  
pombe

JOURNAL Unpublished (1998)  
COMMENT Contact: Mitsuoki Morimyo

Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.

FEATURES  
source Location/Qualifiers

```
1..20
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc02339"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/notes="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
```

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 7113 ATGAATTAATCTTCTCTGTG 7131  
Db 1 ATNAATTCCTTCTCTGTG 19

RESULT 1524

AZ303903

LOCUS AZ303903 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0003B18R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0003B18 R, genomic survey sequence.

ACCESSION AZ303903  
VERSION AZ303903.1 GI:10339339

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: B column: 18  
Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source Location/Qualifiers

1..20

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0003B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5723 CTTTGCTGCTTCTCTTT 5740  
Db 1 CTGTTCTGCTTCTTT 18

RESULT 1525

AZ426873

LOCUS AZ426873 20 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0208L05R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0208L05 R, genomic survey sequence.

ACCESSION AZ426873

VERSION AZ426873.1 GI:10550886

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: L column: 05  
Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source Location/Qualifiers

1..20

/organism="Mus musculus"



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/strain="C57BL/6J"
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/clone="UGGCTM0208L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACCTTTTCTTTTCTTTT 4479  
DB 18 ACATCTTTTCTTTTCTTTT 1

RESULT 1526  
LOCUS AZ772040 20 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M057461R Mouse 10kb plasmid UGGC1M library Mus musculus genomic  
ACCESSION AZ772040  
VERSION AZ772040.1 GI:12894936  
KEYWORDS GSS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0574 row: G column: 11  
Seq primer: CACACAGAAACAGCTATGACC  
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High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
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/mol\_type="genomic DNA"

FEATURES  
source

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/db_xref="taxon:10090"
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/clone_1ib="Mouse 10kb plasmid UGGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4477 TTTTTCCTTGAGACA 4494  
DB 2 TTTTTCCTTGAGACA 19

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LOCUS AZ943793 20 bp DNA linear GSS 26-APR-2001  
DEFINITION 2M020407R Mouse 10kb plasmid UGGC2M library Mus musculus genomic  
ACCESSION AZ943793  
VERSION AZ943793.1 GI:13808082  
KEYWORDS GSS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0204 row: A column: 07  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"

FEATURES  
source

/db\_xref="taxon:10090"  
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/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5435 AGCTTTGGGCATGACAA 5452  
Db 20 AGCTTTGGGTATGATATA 3

## RESULT 1528

AZ428877 21 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M021N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M021N07 R, genomic survey sequence.

ACCESSION AZ428877  
VERSION AZ428877.1 GI:10552986

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

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Unpublished (2000)

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84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0212 row: N column: 07

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

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/mol\_type="genomic DNA"

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/db\_xref="taxon:10090"

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6050 TTTCCTCATTCCTTTT 6067  
Db 4 TTTCCTCTTCCTTTT 21

## RESULT 1529

AZ451384 21 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0250D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0250D13 R, genomic survey sequence.

ACCESSION AZ451384  
VERSION AZ451384.1 GI:10607133

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0250 row: D column: 13

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

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/clone="UUGC1M0250D13"

/sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42n, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3627 GGGGGTGGGAGAGAGCT 3644  
 |||||  
 Db 2 GGGGGTGGGAGAGAGCT 19

RESULT 1530  
 AZ512534/C

LOCUS AZ512534 21 bp DNA linear GSS 05-OCT-2000  
 DEFINITION 1M0358B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0358B07 F, genomic survey sequence.

ACCESSION AZ512534  
 VERSION AZ512534.1 GI:10693850

KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0358 row: B column: 07  
 Seq primer: CATTGTAAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

FEATURES

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 /strain="C57BL/6J"  
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 /sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42n, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGGAGAG 3639  
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 Db 18 GGGGGGGGGGTGGGAGTG 1

RESULT 1531  
 AZ995847

LOCUS AZ995847 21 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0281N16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0281N16 R, genomic survey sequence.

ACCESSION AZ995847  
 VERSION AZ995847.1 GI:13867074

KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0281 row: N column: 16  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

FEATURES

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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0281N16"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

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/clone_11b="Mouse 10Kb plasmid UNGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      3617  GGAATGGGCTGGGCTGG 3634
         |||||
         4  GGTAGGGGCTGGGCTGG 21

RESULT 1533
LOCUS      A1707945      22 bp      mRNA      linear      EST 04-JUN-1999
DEFINITION a644g10.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2319138 3 similar to TR:Q62106 Q62106 PROLINE-RICH SALIVARY
PROTEIN; contains element MSRI repetitive element ;, mRNA sequence.
A1707945
ACCESSION  A1707945.1 GI:4997721
VERSION     EST.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
Hillier,L., Allent,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kizman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Matra,M.,
Martin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F.,
Teisling,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -40UP from Gldco
High quality sequence stop: 1.
location/Qualifiers
1..22
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2319138"
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/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/clone_11b="Barstead aorta HPLRB6"
/note="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a

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modified polylinker; site 1: EcoRI; site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCAGAACTCGACGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTGCGATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."

Query Match      0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2996  GTCCCCCACCCTCACC 3013
         |||||
         5  GCCCCCCACCCTCACC 22

RESULT 1533
LOCUS      A1738599      22 bp      mRNA      linear      EST 21-DEC-1999
DEFINITION w139902.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2392658 3'
similar to SW:MNT_HUMAN Q99583 MAX BINDING PROTEIN MNT ;contains
MER22.ct1 MSRI repetitive element ;, mRNA sequence.
A1738599
ACCESSION  A1738599.1 GI:5100580
VERSION     EST.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 383 Std Error: 0.00
Seq primer: -40UP from Gldco
High quality sequence stop: 1.
location/Qualifiers
1..22
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/clone="IMAGE:2392658"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_11b="NCI_CGAP-Col6"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; site 1: Not I; site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Col6 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

```

Oy 2998 CCCCCACCCCTCACCCCA 3015  
Db 4 CCCCACACCTCTCACCCGA 21

## RESULT 1534

AZ307559 22 bp DNA 1linear GSS 29-SEP-2000  
LOCUS AZ307559  
DEFINITION 1M0009020F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0009020 F, genomic survey sequence.  
ACCESSION AZ307559  
VERSION AZ307559.1 GI:10346680  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: O column: 20  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

Location/Qualifiers

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/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4460 GGAGCTTTTTTTTTTTT 4477  
Db 2 GGAGCTTTTTTTTTTTT 19

## RESULT 1535

AZ345528 22 bp DNA 1linear GSS 29-SEP-2000  
LOCUS AZ345528  
DEFINITION 1M0080N03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0080N03 F, genomic survey sequence.  
ACCESSION AZ345528  
VERSION AZ345528.1 GI:10424765  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: N column: 03  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UGCGIM0080N03"  
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/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
6682 TTATTTTATTTATATAT 6699

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Db          5  TTATTTTATTATTCAT 22
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RESULT 1536
TA214D07P      22 bp  DNA      linear  GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 214D07, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL479490
VERSION        AL479490.1  GI:11845241
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
               Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
               Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus,
               Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/Projects/T_brucei/.
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Best Local Similarity 88.9%; Pred.No.1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy          4460 GGACTTTTTTTTTTTT 4477
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Db          5 GGGGTTTTTTTTTTTTT 22
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RESULT 1537
TA282D06P      22 bp  DNA      linear  GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 282D06, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL487877
VERSION        AL487877.1  GI:11852548
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
               Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
               Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
               Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus,
               Hinxton, project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

```

```

COMMENT        Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
               Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/Projects/T_brucei/.
               Location/Qualifiers
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                 /mol_type="genomic DNA"
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FEATURES
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Query Match          0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred.No.1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy          4460 GGACTTTTTTTTTTTT 4477
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Db          18 GGGGTTTTTTTTTTTTT 1
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RESULT 1538
AM327613      26 bp  mRNA      linear  EST 28-JAN-2000
LOCUS          dq01D09.y1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA
DEFINITION     sequence.
ACCESSION      AM327613
VERSION        AM327613.1  GI:6798108
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
               1 (bases 1 to 26)
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
               Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgabs-r@mail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Edge Biosystems
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNL at:
               www-bio.1nl.gov/bdrp/image/image.html
               Plate: LNCM0028 row: C column: 17
               Seq primer: M13RPI reverse primer (ABI).
               Location/Qualifiers
                 1..26
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                 Edge Biosystems."

FEATURES
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Best Local Similarity 73.1%; Pred.No.2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 4012 AAAATGAGAAAAAGAGAAACAA 4037  
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 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1539  
 CF278359/c 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa cDNA clone 14ETL--04-D22, mRNA sequence.  
 ACCESSION CF278359  
 VERSION CF278359.1 GI:33655745  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /organism="Oryza sativa"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAA 4037  
 ||||| ||||| ||||| ||||| |||||  
 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1540  
 CF282426 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--09-P01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa cDNA clone 14ETL--09-P01, mRNA sequence.  
 ACCESSION CF282426  
 VERSION CF282426.1 GI:336559813  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /tissue\_type="leaf"  
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 /lab\_host="E.coli DH10B"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAA 4037  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1541  
 CF297087 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 30DGS--07-L18.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa cDNA clone 30DGS--07-L18, mRNA sequence.  
 ACCESSION CF297087  
 VERSION CF297087.1 GI:33666120  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
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 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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Query Match 0.2%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

# RESULT 1542

CF329701/c

LOCUS 26 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF329701  
 VERSION CF329701.1 GI:33671462

KEYWORDS EST.  
 SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

source

1..26  
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 with oligoribonucleotides and then used as templates for  
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Query Match 0.2%; Score 14.8; DB 1; Length 26;  
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 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1543  
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 LOCUS 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--08-M19, mRNA sequence.  
 ACCESSION CF302874  
 VERSION CF302874.1 GI:33674635  
 KEYWORDS EST.  
 SOURCE Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
 COMMENT Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

source

1..26  
 /organism="Oryza sativa"  
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 /lab\_host="E.coli DH10B"  
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 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1544  
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 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--06-J01, mRNA sequence.  
 ACCESSION CF311369  
 VERSION CF311369.1 GI:33683130  
 KEYWORDS EST.  
 SOURCE Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 1 (bases 1 to 26)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

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1..26  
 /organism="Oryza sativa"  
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 /clone\_1b="ABF3-overexpressing transgenic rice plasmid  
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 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Leaf was dried  
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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1545  
CF331439/c 26 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) Oryza

ACCESSION CF331439  
VERSION CF331439.1 GI:33811097  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)  
Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

AUTHORS Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of BioScience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
source Location/Qualifiers

1..26  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL-07-002"  
/cissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1546  
AZ359871

LOCUS AZ359871 26 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0102423R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0102423 R, genomic survey sequence.

ACCESSION AZ359871.1 GI:10473571  
VERSION AZ359871.1  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

# REFERENCE

1. (bases 1 to 26)  
Dunn,D., Royagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

# JOURNAL

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 1000 Std Error: 0.00  
Plate: 0102 row: H column: 23  
Seq primer: CACACGAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

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source Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0102423"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g1/4732114[9b]/AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1547  
AZ376664

LOCUS AZ376664 26 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0130808R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0130808 R, genomic survey sequence.

ACCESSION AZ376664.1 GI:10490364  
VERSION AZ376664.1  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: E column: 08  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

FEATURES

source

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Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0130E08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03; 7; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 7;

Qy 4012 AAATGAGAAAAAGAGAGAAACAA 4037  
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1548

AZ389765

LOCUS AZ389765 26 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0150D13R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0150D13 R, genomic survey sequence.

ACCESSION AZ389765

VERSION AZ389765.1 GI:10503473

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0150 row: D column: 13  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

FEATURES

source

1..26

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0150D13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03; 7; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 7;

Qy 4012 AAATGAGAAAAAGAGAGAAACAA 4037  
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1549

AZ414673

LOCUS AZ414673 26 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0189M07F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0189M07 F, genomic survey sequence.

ACCESSION AZ414673

VERSION AZ414673.1 GI:10538686

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Issail, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert length: 10000 Std Error: 0.00  
Plate: 0189 row: M column: 07  
Seq primer: CGTTCGAAAACACCGCCACT  
Class: plasmid ends  
High quality sequence stop: 26.

**Source**

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT	1550			
	AZ593300			
LOCUS	AZ593300	26 bp	DNA	linear
DEFINITION	M04040E1C1R Mouse 10kb plasmid UUEC1M library Mus musculus genomic			
	clone UUEC1M0404E16 R, genomic survey sequence.			
ACCESSION	AZ593300			
VERSION	AZ593300.1	GI:11715490		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			

1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0405 row: E column: 16  
Seq primer: CACACAGGAAACGCTATACAC  
Class: Plasmid ends  
High quality sequence: 26.

Query Match	0.2%	Score 14.8;	DB 1;	length 26;
Best Local Similarity	73.1%;	Pred. No. 2e+03;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

RESULT 1551	
AZ612722/c	
LOCUS	AZ612722
DEFINITION	26 bp DNA linear GSS 13-DEC-2000
ACCESSION	U0039517R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION	clone UUGC1M0439E17 R, genomic survey sequence.
KEYWORDS	AZ612722
SOURCE	AZ612722.1 GI:11734912
ORGANISM	GSS.
	Mus musculus (house mouse)
	Mus musculus

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE	Niederhausem,A. and Wright,D,Weiss,R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT	plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0439 row: E column: 17 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 26. Location/Qualifiers 1..26
FEATURES	
source	

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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UTGICM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrotamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (gill473211[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1). The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

[illegible]

RESULT	1552
AZ624441/c	
LOCUS	AZ624441          26 bp    DNA        linear     GSS 13-DEC-2000
DEFINITION	1M046307F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M046307 F, genomic survey sequence.
ACCESSION	AZ624441
VERSION	AZ624441.1
KEYWORDS	GI:11746631
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ismail,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
AUTHORS	

Mouse whole-genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0463 row: G column: 07  
Seq primer: CGTGTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

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 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1fb="Mouse 10kb plasmid U9CIG library"  
 /note="Vector: PWD242X; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD2 (gl1473211.4[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor-vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match	0.25	Score 14.8	DB 1	Length 26
Best Local Similarity	73.1%	Pred. No. 2e+03		
Matches 19; Conservative	0	Mismatches	7	Indels 0; Gaps 0;
Qy	4012	AAATGAGAAAAAGAGAAACCA	4037	
Db	26	AAAAAAAAAAAAAAAAAAAAA	1	

RESULT	1553				
LOCUS	AZ627846/c				
DEFINITION	AZ627846	26 bp	DNA	linear	GSS 13-DEC-2000
ACCESSION	U0047H08F	Mouse 10kb plasmid U00GCM library	Mus musculus genomic clone	U00GCM047AH08 F,	genomic survey sequence.
VERSION	AZ627846				
KEYWORDS	AZ627846.1	GI:11750132			
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26) Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedenhuisern,A. and Wright,D.,Weise,K., Mouse whole genome scaffolding with paired end reads from 10kb				
TITLE					

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: H column: 08  
Seq primer: CAGTGTAAACAGCAGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1b="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 1554

AZ80453/C

LOCUS 26 bp DNA linear GSS 14-DEC-2000  
DEFINITION 1M0525H1SR Mouse 10kb plasmid UGC1M library Mus musculus genomic  
clone UGC1M0525H1S R, genomic survey sequence.

ACCESSION

AZ80453

VERSION AZ80453.1 GI:11789108

KEYWORDS

GSS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0525 row: H column: 15  
Seq primer: CACACAGAAACAGCATATAC  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1b="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAGAGAAACAA 4037  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

## RESULT 1555

AZ800453

LOCUS 26 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0058023F Mouse 10kb plasmid UGC1M library Mus musculus genomic  
clone UGC2M0058023 F, genomic survey sequence.

ACCESSION

AZ800453

VERSION AZ800453.1 GI:12952583

KEYWORDS

GSS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah  
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0058 row: 0 column: 23  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

## source

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1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M058023"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.24; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.14; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1556  
AZ963974/c 26 bp DNA linear GSS 27-APR-2001  
LOCUS 2M023N01F Mouse 10kb plasmid UUC2M library Mus musculus genomic  
clone UUCG2M023N01 F, genomic survey sequence.  
ACCESSION AZ963974  
VERSION AZ963974.1 GI:13835201  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0233 row: N column: 01  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

## source

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1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0233N01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.24; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.14; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1557  
TA324D07P 26 bp DNA linear GSS 13-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 324d07, forward sequence,  
genomic survey sequence.  
ACCESSION AL493390  
VERSION AL493390.1 GI:11867755  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 26)  
AUTHORS Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
TITLE Direct Submision  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
n1@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrel, Oxford University Press, 1999).

Email: nelseyed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1..26

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

/db\_xref="taxon:5691"

/clone="324d07"

Query Match Best Local Similarity 0.2%; Score 14.8; DB 1; Length 26;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAAAACAA 4037

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

## RESULT 1558

AZ355083

LOCUS

DEFINITION 1M0094D14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0094D14 R, genomic survey sequence.

ACCESSION AZ355083.1 GI:10467134

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0094 row: D column: 14

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0094D14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match Best Local Similarity 0.2%; Score 14.8; DB 1; Length 26;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAAAAACAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

## RESULT 1559

AZ623156/c

LOCUS

DEFINITION 1M0460L01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0460L01 R, genomic survey sequence.

ACCESSION AZ623156.1 GI:11745346

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: L column: 01

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0460L01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson





University of Utah Genome Center  
 University of Utah  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0243 row: N column: 14  
 Seg primer: CACACAGAAACAGCTATGAC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers

## FEATURES

source

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1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0243N14"
/sex="female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"/
/clone_1lb="Mouse 10kb plasmid UGC2M library"
/notes="Vector: pMD29v. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match Best Local Similarity 0.2%; Score 14.8; DB 1; Length 27;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAA 4037

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1563

NS1845/c

LOCUS 27 bp mRNA linear EST 30-JAN-1997  
 DEFINITION Y202d07.s1 Soares multiple sclerosis 2NbhMSP Homo sapiens CDNA  
 clone IMAGE:281865 3' similar to gb:U53463 SRUM RESPONSE FACTOR  
 ACCESSION Y202d07.1 (HUMAN); mRNA sequence.

VERSION NS1845

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 27)  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

AUTHORS

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478  
 PUBMED 8889549

COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estowatson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 450 Std Error: 0.00  
 Seg primer: m3 -40 forward  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

source

```

1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3900397"
/db_xref="taxon:9606"
/clone="IMAGE:281869"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares multiple sclerosis 2NbhMSP"
/notes="Vector: pT73D (Pharmacia) with a modified polylinker V type: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCCATCGAGTGGAGGCGCCGATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Benito Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."

```

Query Match Best Local Similarity 0.2%; Score 14.8; DB 1; Length 27;

Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 27 AAATTTTAAAAA 1

RESULT 1564

T52836/c

LOCUS 28 bp mRNA linear EST 06-FEB-1995  
 DEFINITION Y481b09.s1 Stratagene ovary (#937217) Homo sapiens CDNA  
 IMAGE:68057 3' similar to gb:U53463 GLUTATHIONE  
 PEROXIDASE-GASTROINTESTINAL (HUMAN); mRNA sequence.

VERSION T52836

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 28)  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

AUTHORS

TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478

**PUBMED  
COMMENT**

8889549  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [grcw@wustl.edu](mailto:grcw@wustl.edu)  
Insert Size: 51

High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNM. This clone is available royalty-free  
through LNM; contact the IMAGE Consortium (info@image.lnm.gov)  
for further information. Trace considered overall poor quality  
Insert Length: 51 Std Error: 0.00

High quality sequence stop: 1  
Location/Qualifiers

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1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:504314"
/db_xref="EAXON:9606"
/clone="IMAGE:68057"
/sex="female"
/dev_stage="49 year old"
/lab_host="SO4R cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAAATTCGACACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' "
```

Query Match	0.2%	Score 14.8;	DB 1;	length 28;
Best Local Similarity	73.1%;	Pred. No. 2.1e+03;		
Matches 19;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	4012	AAATGAGAAAAAGAGAGAAAACAA	4037
Db	26	AAAAACAAAAA	1

RESULT	1565
A2819924	
LOCUS	A2819924 29 bp DNA linear GSS 20-FEB-2001
DEFINITION	2M0091A19R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0091A19 R, genomic survey sequence.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 29)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

Class: plasmid ends	High quality sequence stop: 29
Location/Qualifiers	1. .29

1. 29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0091A19"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1fb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD229; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (<http://47321419b/AT29072.11>), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.2%	Score 14.8	DB 1	Length 29
Best Local Similarity	73.1%	Pred. No. 2.1e+03		
Matches 19	Conservative 0	Mismatches 7	Indels 0	Gaps 0

QY	4012	AAAAATGAGAAAAAAAAAGAGAGAAACAA	4037
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	26

RESULT	1566				
AZ492630/c					
LOCUS	AZ492630	29 bp	DNA	linear	GSS 05-OCT-2000
DEFINITION	1M0326B22 Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0326B22 R, genomic survey sequence.				

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	Plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 plate: 0326 row: B column: 22 Seq primer: CACACAGGAAACAGCTATTGACC Class: plasmid ends



```

SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1..29
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="7LEAF--05-E15"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.2%; Score 14.8; DB 1; Length 29;
Best Local Similarity 73.1%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4014 AATGAGAAAAAGAGACAAACAAA 4039
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        26 AAGCGTAAAAAAGAGAAAAA 1

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DEFINITION 30DGS--05-E14.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-E14, mRNA sequence.
ACCESSION  CF295370
VERSION     CF295370.1 GI:33664403
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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            RT-PCR."

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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4020 AAAAAAGAGAAAAACAAATGTTAT 4045
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LOCUS      CF293772      29 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--03-B05.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--03-B05, mRNA sequence.
ACCESSION  CF293772
VERSION     CF293772.1 GI:33662805
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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KEYWORDS  
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Oryza sativaEukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 31)  
Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,  
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/QualifiersFEATURES  
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DB 29 AAAAAAAAAAAAAACACTGTCTAT 4RESULT 1573  
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DEFINITION ABF--08-H15.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--08-H15, mRNA sequence.  
ACCESSION CF312635  
VERSION CF312635.1 GI:33684396  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 31)  
Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,  
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/QualifiersFEATURES  
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line."Query Match 0.2%; Score 14.8; DB 1; Length 31;  
Best Local Similarity 73.1%; Pred. No. 2.2e+03;  
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DB 30 AAAAAAAAAAAAAACACTGTCTAT 5RESULT 1574  
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DEFINITION BX551140 Glossina morsitans moritans adult infected gut Glossina  
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VERSION BX551140.1 GI:33374994  
KEYWORDS EST.  
SOURCE Glossina morsitans moritans  
ORGANISM Glossina morsitans moritans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
1 (bases 1 to 33)  
Lehane, M.-J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,  
Hamilton, D., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans moritans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22861942  
14519198

## COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix g1c are reverse primer reads starting at 5'  
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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAGAGAAACCA 4037  
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RESULT 1575  
 BXS66898/c  
 LOCUS  
 DEFINITION BXS66898 Glossina morsitans morsitans adult infected gut Glossina  
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 VERSION BXS66898.1 GI:33433863  
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 33)  
 Lehane, M.J., Akcoy, S., Gibson, W., Kertou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*  
*morsitans morsitans* and expression analysis of putative immune  
 response genes  
 Genome Biol. 4 (10), R63 (2003)  
 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
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Qy 4012 AAATGAGAAAAGAGAAACCA 4037  
 Db 33 AAAACAAAAAATACTA 8

RESULT 1576  
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 14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 Oryza sativa cDNA clone 14ETL--01-N19, mRNA sequence.  
 ACCESSION CP276638  
 VERSION CP276638.1 GI:33654024  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Oryza sativa

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 ACCESSION A2597932.1 GI:11720122  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D. Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 High quality sequence stop: 21.

FEATURES  
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Query Match 0.2%; Score 14.6; DB 1; Length 21;  
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Qy 4012 AAAATGAGAAAAAGAGAGA 4032  
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21 AAAAAAAAAAAAAAAAAA 1

RESULT 1578 21 bp mRNA linear EST 14-ANG-2003  
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DEFINITION 14ETL--07-M14, b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
ACCESSION CF280925  
VERSION CF280925.1 GI:33658311  
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SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioesence and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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ACCESSION AZ339966  
VERSION AZ339966.1 GI:10414760  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iselm,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tilney,A., von Niederhausen,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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High quality sequence step: 21.  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

FEATURES  
source

with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%	Score 14.6	DB 1	Length 21
Best Local Similarity	81.0%	Pred. No. 1.6e+03		
Matches 17	Conservative 0	Mismatches 4	Indels 0	Gaps 0
QY	4465	TTTTTTTTTTTTTTTTTGT	4485	
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RESULT	1580
LOCUS	AZ394897
DEFINITION	AZ394897 21 bp DNA linear GSS 03-OCT-2000
ACCESSION	U01581H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION	clone UUGC1M015811 R, genomic survey sequence.
KEYWORDS	AZ394897.1 GI:10509969
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 21) Dunn, P., Aoyagi, A., Barber, M., Bascom, T., Duval, B., Hamil, C., Isslam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0158 row: H column: 11 Seq primer: CACACAGAAACAGCTAAGACC Class: plasmid ends High quality sequence stop.21.
JOURNAL COMMENT	

purified. The sheared, adapted mouse DNA was annealed to the adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%	Score 14.6	DB 1	Length 21
Best Local Similarity	8.0%	Pred. No. 1.6e+03		
Matches	17	Conservative	0	Mismatches 4; Indels 0; Gaps 0;
OY	5327	TCTCTTTGGCTCACTCTCT	5347	
Db	1	TCTCTCTCTCTCTCTCTCT	21	

RESULT	1581
AZ419284/c	
LOCUS	AZ419284          21 bp    DNA        linear    GSS 03-OCT-2000
DEFINITION	IM0195A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION	clone UUGC1M0195A16 R, genomic survey sequence.
VERSION	AZ419284
KEYWORDS	AZ419284.1   GI:10543297
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eumaxyoti; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murine; Mus. 1 (bases 1 to 21) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Tallam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10xb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000     Std Error: 0.00 Plate: 0195     row: A     column: 16 Seq primer: CACAOCAGGAACACACTTGACC Class: plasmid ends High quality sequence stop: 21.
JOURNAL COMMENT	

<http://www.jaxx.org/resources/documents/dnaase/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi1473211|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and



adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGCTGGGGTGGAGAGCAG 3642  
DB 21 GGGGGGGGGGGGGGGGGG 1

## RESULT 1582

AZ483617 21 bp DNA linear GSS 05-OCT-2000  
LOCUS AZ483617/c  
DEFINITION IM0309A05R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0309A05 R, genomic survey sequence.

ACCESSION AZ483617  
VERSION AZ483617.1 GI:10647772

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0309 row: A column: 05

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG1M0309A05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4468 TTTTGTGTTTGTGTTT 4488  
DB 21 TTTTGTGTTTGTGTTT 1

## RESULT 1583

AZ499846 21 bp DNA linear GSS 05-OCT-2000  
LOCUS AZ499846/c  
DEFINITION IM0337E23R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0337E23 R, genomic survey sequence.

ACCESSION AZ499846  
VERSION AZ499846.1 GI:10679079

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0337 row: E column: 23

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG1M0337E23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells



Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 5327 TCTCTCTTGGCTCACTCTCT 5347  
Db 21 TCTCTCTCTCTCTCTCTCTCT 1

## RESULT 1586

A2627978

LOCUS

DEFINITION A2627978 21 bp DNA linear GSS 13-DEC-2000  
1M0476L04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0476L04 F, genomic survey sequence.

ACCESSION

A2627978

VERSION

A2627978.1 GI:11750168

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT/  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plates: 0476 Row: L Column: 04  
Seq primer: CCGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

## FEATURES

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1.21  
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/clone="UUGCLM0476L04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 5327 TCTCTCTTGGCTCACTCTCT 5347  
Db 1 TCTCTCTCTCTCTCTCTCTCT 21

## RESULT 1587

A2770188/c

LOCUS

DEFINITION A2770188 21 bp DNA linear GSS 16-FEB-2001  
1M0571A12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0571A12 R, genomic survey sequence.

ACCESSION

A2770188

VERSION

A2770188.1 GI:12891111

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT/  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plates: 0571 Row: A Column: 12  
Seq primer: CACACAGAAACGCTATGAC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

## FEATURES

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/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUGCLM0571A12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.2%; Score 14.6; DB 1; Length 21;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3004 CCCCTACCCCATCTGTGCAC 3024  
 Db 21 CCCCTCCCCCATGTATGCAC 1

RESULT 1588  
 AZ961893/c 21 bp DNA linear GSS 27-APR-2001  
 LOCUS 2M0230E06R Mouse 10kb plasmid UGCG2M library Mus musculus genomic  
 DEFINITION clone UGCG2M0230E06 R, genomic survey sequence.  
 ACCESSION AZ961893  
 VERSION AZ961893.1 GI:13833120  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0230 row: E column: 06  
 Seq primer: CACACAGCAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
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 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCG2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 1.6e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGAGAGAG 3642  
 Db 21 GGGGGGGGGGGGGGGGGG 1

RESULT 1589  
 AZ374487 22 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0127H16F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 DEFINITION clone UGCG1M0127H16 F, genomic survey sequence.  
 ACCESSION AZ374487  
 VERSION AZ374487.1 GI:10488187  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0127 row: H column: 16  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 22.

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0127H16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4019 GAAAAAGAGAGAAAAA 4039  
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 Db 1 GAAAAAGAGAGAAAAA 21

RESULT 1590  
 A1439277 22 bp mRNA linear EST 09-MAR-1999  
 LOCUS t154602.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134250 3'  
 DEFINITION similar to TR:Q17089 Q17089 COLLAGEN; contains element MER22  
 repetitive element ;, mRNA sequence.

ACCESSION A1439277  
 VERSION A1439277  
 KEYWORDS GI:4303196  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 22)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Life Technologies catalog #: 11547-015  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bpr/image/image.html](http://www.bio.llnl.gov/bpr/image/image.html)

Trace considered overall poor quality  
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 High quality sequence stop: 1.  
 Location/Qualifiers  
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 Oligo dt. Average insert size 1.25 kb. Life Technologies  
 catalog #: 11547-015"

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3390 CCAGCTGCACCCGCCACCTT 3410  
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 Db 1 CCCGCCGCCACCCGCCCTT 21

RESULT 1591  
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 DEFINITION A1439277 3'-directed mouse cDNA library Mus musculus cDNA clone  
 BED0016802 3', mRNA sequence.  
 ACCESSION A1439277  
 VERSION A1439277  
 KEYWORDS GI:20327801  
 SOURCE EST.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 Kato, K. and Matoba, R.  
 Generation of expressed sequence tags from mouse brain

JOURNAL  
 COMMENT Unpublished (2002)  
 Contact: Kikuya Kato  
 Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: [kkato@bs.nara.ac.jp](mailto:kkato@bs.nara.ac.jp)  
 URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="BED0016802"  
 /tissue\_type="brain"  
 /clone\_lib="3'-directed mouse cDNA library"

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1531 TTCTACATGGATGATGATC 1551  
 |||||  
 Db 21 TTCTACATGATGATGATC 1

RESULT 1592  
 A2447246 22 bp DNA linear GSS 04-OCT-2000  
 LOCUS A2447246/c  
 DEFINITION 1M0244E23F Mouse 10kb plasmid UUGCM library Mus musculus genomic  
 clone UUGCM0244E23 F, genomic survey sequence.  
 ACCESSION A2447246  
 VERSION A2447246  
 KEYWORDS GSS.  
 SOURCE 1..22  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D. Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0244 row: E column: 23  
 Seq primer: CGTTCGAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 22.  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Cy 3623 GGGTGGGGGTGGAGAGGAGG 3643  
Db 22 GGGGGGGGGGGGGGGGGGGG 2

## RESULT 1593

AZ464354 22 bp DNA linear GSS 04-OCT-2000

LOCUS 1M0273M1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0273M1 R, genomic survey sequence.

ACCESSION AZ464354

VERSION AZ464354.1 GI:10622479

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: M column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

FEATURES

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0273M1"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Cy 5326 TTCTCTCTTGGCCCTCACTCTC 5346  
Db 2 TTCTCTCTCTCTCTCTCTC 2

## RESULT 1594

AZ611419/c

LOCUS 1M0437D1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0437D1 R, genomic survey sequence.

ACCESSION AZ611419

VERSION AZ611419.1 GI:11733609

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0437 row: D column: 15

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

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/organism="Mus musculus"

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/strain="C57BL/6J"

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/clone="UUGC1M0437D1"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3623 GGGTGGGGGTGGGAGAGAGG 3643  
Db 22 GGGGGGGGGGGGGGGGGGGG 2

RESULT 1595  
LOCUS AZ766712/c 22 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0564A03R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0564A03 R, genomic survey sequence.

ACCESSION AZ766712  
VERSION AZ766712.1 GI:12884063  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: A column: 03  
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Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGTGGGGGTGGGAGAGAGG 3642  
Db 21 GGGGTGGGGGGGGGGGGGGG 1

RESULT 1596  
LOCUS AZ769521/c 22 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0570018F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0570018 F, genomic survey sequence.

ACCESSION AZ769521  
VERSION AZ769521.1 GI:12889741  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0570 row: O column: 18  
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Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adopted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adopted mouse DNA was annealed to adopted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3623 GGGTGGGGGTGGGAGAGAGG 3643  
DB 22 GGGGGGGGGGTGGGGGGGGG 2

RESULT 1597  
A2776605/c 22 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0010119F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0010119 F, genomic survey sequence.

ACCESSION A2776605  
VERSION A2776605.1 GI:12904372  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: 1 column: 19  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

#### FEATURES

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adopted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adopted mouse DNA was annealed to adopted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 55 GGCACGAGAGCTGCGGGGCG 75  
DB 22 GGGAACGACGAGCTGAGGAGC 2

RESULT 1598  
A2778745 22 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0014M08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0014M08 F, genomic survey sequence.

ACCESSION A2778745  
VERSION A2778745.1 GI:12908699  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0014 row: M column: 08  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

#### FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0014M08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The



adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5885 CCTTACTGCAAGAACCAAG 5905  
DB 1 CCTTGACTACAGAAATCAAG 21

## RESULT 1599

LOCUS AZ868780 22 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0180E12R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
ACCESSION AZ868780  
VERSION AZ868780.1 GI:13072436  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (baes 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0180 row: E column: 12  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

## FEATURES

1. 22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0180E12"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3615 GGGGAATGGGCTGGGCTGGG 3635  
DB 2 GGGGTTGGGGGTAGGGGTGGG 22

## RESULT 1600

LOCUS AZ958390 22 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0225J07R Mouse 10kb plasmid UGCG2M library Mus musculus genomic  
ACCESSION AZ958390  
VERSION AZ958390.1 GI:13829617  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (baes 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0225 row: J column: 07  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

## FEATURES

1. 22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0225J07"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3615 GGGGATGGGGTGGGGTGGG 3635  
Db 21 GGGGATTTGGGGGGGGGGG 1

RESULT 1601  
AZ974046/c  
LOCUS 22 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M024GC01R Mouse 10kb plasmid U0GC2M library Mus musculus genomic  
clone U0GC2M024GC01 R, genomic survey sequence.  
ACCESSION AZ974046  
VERSION AZ974046.1 GI:13845273  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
Dunn, P., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamill, C.,  
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellin, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Nederhauser, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0248 row: C column: 01  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U0GC2M024GC01"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U0GC2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3622 GGGGTGGGGTGGAGAGAGAG 3642  
Db 21 GGGGGGGGGGGGGGGGGGAG 1

RESULT 1602  
TA8C02P  
LOCUS 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 8c02, forward sequence, genomic  
survey sequence.  
ACCESSION AL452598  
VERSION AL452598.1 GI:11861142  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 22)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajadream, M.A. and Barrell, B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

FEATURES  
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1..22  
/organism="Trypanosoma brucei"  
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/db\_xref="taxon:5691"  
/clone="8c02"

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3652 TCCCTTTCTCCTTATCTCTCC 3872  
Db 2 TCCCTTTGCCATATCTCTCC 22

RESULT 1603  
AZ380872  
LOCUS 23 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0137H02P Mouse 10kb plasmid U0GC1M library Mus musculus genomic  
clone U0GC1M0137H02 F, genomic survey sequence.  
ACCESSION AZ380872

VERSION AZ380872.1 GI:10494572  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iselm, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0137 row: H column: 02  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
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 1. 23  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0137H02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
 Query Match 0.2%; Score 14.6; DB 1; Length 23;  
 Best Local Similarity 81.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4031 AAAACAAATGTTATTTTAT 4051  
 DB 22 AAAAAAAAAATTTTTTTTTT 2  
 RESULT 1604  
 AZ514388/c 24 bp DNA linear GSS 05-OCT-2000  
 LOCUS AZ514388  
 DEFINITION IM0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0361H04 F, genomic survey sequence.  
 ACCESSION AZ514388  
 VERSION AZ514388.1 GI:10695704

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iselm, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0361 row: H column: 04  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.  
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 source Location/Qualifiers  
 1. 24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0361H04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
 Query Match 0.2%; Score 14.6; DB 1; Length 24;  
 Best Local Similarity 81.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4013 AATGAGAAAAAGAGAAA 4033  
 DB 24 AAAAAAAAAAAAAAAAAAGAGAAA 4  
 RESULT 1605  
 AZ485624 26 bp DNA linear GSS 05-OCT-2000  
 LOCUS AZ485624  
 DEFINITION IM0313H1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0313H1 F, genomic survey sequence.  
 ACCESSION AZ485624  
 VERSION AZ485624.1 GI:10651606

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0313 row: H column: 11  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

FEATURES

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1..26  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gbl|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 26;  
Best Local Similarity 81.0%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAAACAAAT 4040  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAT 21

RESULT 1606

LOCUS CF639306 26 bp mRNA linear EST 02-OCT-2003

DEFINITION D14 A02 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA sequence.

ACCESSION CF639306

VERSION CF639306.1 GI:37403783

KEYWORDS EST.

SOURCE Ustilago maydis

ORGANISM Ustilago maydis

REFERENCE Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago. 1 (bases 1 to 26)

AUTHORS Nugent, K.G., Choife, K. and Saville, B.J.

TITLE Gene Expression during Ustilago maydis Diploid Filamentous Growth: EST Library Creation and Analyses

JOURNAL Unpublished (2003)

COMMENT Contact: Barry J. Saville  
Saville Lab  
University of Toronto  
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada  
Tel: 905 569 4702  
Fax: 905 828 3792  
Email: bsaville@utmsc.utoronto.ca  
Plate: UTM-UM-D126/7-014-UTM row: 02 column: A  
Seq primer: T7 Reverse (5' GAGTAAATACACTACTATAGG 3')  
High quality sequence stop: 26.

FEATURES

source

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/db\_xref="taxon:5270"  
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/clone\_lib="Filamentous Forced Diploid"  
/note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

Query Match 0.2%; Score 14.6; DB 1; Length 26;  
Best Local Similarity 77.3%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAAACAAA 4039  
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Db 4 AAAAAAAAAAAAAAAAAA 25

RESULT 1607

LOCUS T52979/c 27 bp mRNA linear EST 06-FEB-1995

DEFINITION T52979.61 Striatagene ovary (#937217) Homo sapiens cDNA clone IMAGE:68198.3, similar to gp:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR (HUMAN), mRNA sequence.

ACCESSION T52979

VERSION T52979.1 GI:654839

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 27)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisose, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellendberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 8889549

COMMENT Other ESTs: ya82e08.r1  
Contact: Wilbon RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu



TITLE	Large-scale Sequencing Analysis of Rice ESTs									
JOURNAL	Unpublished (2003)									
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.									
FEATURES	Location/Qualifiers									
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Qy	4464	TTTTTTTTTTTTTTT	4479							
Db	1	TTTGTTTTTTTTTTT	16							
Query Match	0.2%; Score 14.4; DB 1; Length 16;									
Best Local Similarity	93.8%; Pred. No. 1e+03;									
Matches	15;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
RESULT 1612										
AM247165										
LOCUS	2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3',									
DEFINITION	mRNA sequence.									
ACCESSION	AM247165									
VERSION	AM247165.1 GI:6590158									
KEYWORDS	EST.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.									
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/									
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL	Unpublished (1999)									
COMMENT	Other ESTs: 2819675.5prime Contact: Robert Strauberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA library Preparation: Ling Hong/Rubin laboratory cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNLI) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: www.bio.lnli.gov/bdrr/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: trace file contained 17 contiguous distinct peaks following vector sequence. Plate: ILICM2 row: D column: 12 High quality sequence stop: 17. Location/Qualifiers									
FEATURES	1. 17									
SOURCE	Location/Qualifiers									

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/mol_type="mRNA"
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/clone_image="2819675"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.2%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464 TTTT TTTT TTTT TTTT TTTT 4479
Db      2 TTTT TTTT GTTTT 17

RESULT 1613
CFJ18426/c      19 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      HD--08-120.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION      CFJ18426
VERSION      CFJ18426.1 GI:33690187
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--08-120"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.2%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      5027 AGGAGCAGCTCAGTG 5042
Db      19 AGGAGCAGCTCACTG 4

RESULT 1614
AZ656129      19 bp      DNA      linear      GSS 14-DEC-2000
LOCUS      1M0531C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0531C04 R, genomic survey sequence.
ACCESSION      AZ656129
VERSION      AZ656129.1 GI:11793275
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0531 row: C column: 04
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence scop: 19.
Location/Qualifiers

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0531C04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gt14732114[gb|AF139072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2042 CAGCAGTGTAAGCAG 2057

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Db 2 CAGCTGTGTAGGCG 17

RESULT 1615  
A2766990/c

LOCUS 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0564H19 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0564H19 R, genomic survey sequence.

ACCESSION A2766990

VERSION A2766990.1 GI:12884624

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: H column: 19

Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

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1. 19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0564H19"
    /sex="Male"
    /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"/
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv, Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (g14732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4463 CTTTCTTTTCTTTT 4478

|||||

Db 16 CATTCTTTTCTTTT 1

RESULT 1616  
A2991606

LOCUS 19 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0275K24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0275K24 R, genomic survey sequence.

ACCESSION A2991606

VERSION A2991606.1 GI:13862833

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0275 row: K column: 24

Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

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1. 19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0275K24"
    /sex="Female"
    /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"/
    /clone_lib="Mouse 10kb plasmid UUGC2M library"
    /note="Vector: PWD42nv, Purified genomic DNA from M.
    musculus C57BL/6J (female) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (g14732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6741 TTTCTTAATCTGATC 6756

Db 1 TTCTTAACATCTGATC 16



## RESULT 1617

AZ368518/c

LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0118G09R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

ACCESSION clone UGCGIM0118G09 R, genomic survey sequence.

KEYWORDS AZ368518

VERSION AZ368518.1 GI:10482218

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Isaiah, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0118 row: G column: 09

Seq primer: CACACAGGAACACGATATGAC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. 20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0118G09"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: pMD229; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD22 (g14732114|9b|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4479

DB 20 TTTT TTTT TTTT TTTT 5

## RESULT 1618

A1748552/c

LOCUS A1748552 22 bp mRNA linear EST 13-DEC-1999

DEFINITION gb544161.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1016-358 5' similar to SW:SP49 HUMAN Q15427 SPLICHSOME

ASSOCIATED PROTEIN 49 /, mRNA sequence.

ACCESSION A1748552

VERSION A1748552.1 GI:5126816

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 22)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, J., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,

Schurr, R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 1.

Location/Qualifiers

1. 22

/organism="Glycine max"

/mol\_type="mRNA"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-358"

/tissue\_type="Immature flowers of field grown plants"

/lab\_host="XL10-Gold"

/clone\_lib="Gm-c1016"

/note="Vector: pBluescript II Xr; Site 1: EcoRI, Site 2:

XhoI; This cDNA library was constructed from mRNA isolated

from immature flowers of field grown plants. The cDNA

library was prepared using the Stratagene pBluescript II

XR library construction kit. Complementary DNA was

synthesized from mRNA using a primer consisting of a poly

(dT) sequence with a XhoI restriction site. EcoRI adaptors

were ligated to the blunt-ended cDNA fragments followed by

XhoI digestion. The cDNA fragments were directionally

cloned into the EcoRI-XhoI restriction site of the

pBluescript vector. The ligated cDNA fragments were

transformed into XL10-Gold host cells. This library was

constructed by Dr. Randy Shoemaker and Dr. John

Erpelting."

Query Match 0.2%; Score 14.4; DB 1; Length 22;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2866 GCAAGAGAGAGAGAGG 2881

DB 16 GGAAGAGAGAGAGAGG 1



84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0560 row: P column: 11  
 Seq primer: CACACAGAAACAGCATATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.

## FEATURES

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1. .24

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U08C1M0560P11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U08C1M library"  
 /note="Vector: PMD42nv. Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passages through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number 941  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 24;  
 Best Local Similarity 75.0%; Pred. No. 2e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4022 AAAAGAGCAAAACAAATGATAT 4045  
 Db 1 AAAAAAAAAAAAAAAAAAATTTT 24

RESULT 1622  
 TA155F120 24 bp DNA 1linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 155f12, reverse sequence,  
 genomic survey sequence.  
 ACCESSION AL472638  
 VERSION AL472638.1 GI:11838089  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 24)  
 Hall, N., Bowman, S., Lemard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Welby, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 mh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (

4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

## FEATURES

source

1. .24

/organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="155f12"

Query Match 0.2%; Score 14.4; DB 1; Length 24;  
 Best Local Similarity 75.0%; Pred. No. 2e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6977 AAAACAAACAAATGAGCTGGG 7000  
 Db 1 AAAAAAAAAAAAAAAAAAGCGCGCGG 24

RESULT 1623  
 AW248929 24 bp mRNA 1linear EST 07-JAN-2000  
 LOCUS 2819212.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819212 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AW248929  
 VERSION AW248929.1 GI:6591922  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 24)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other ESTs: 2819212.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LBNL) DNA Sequencing by: Berkeley MGC sequencing  
 project clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LBNL at:  
 www.bio.lnl.gov/btrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patchwork.pl from Berkeley  
 Proscophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu/low/QualitySequence/10  
 contiguous PHRED high quality bases following vector sequence. Very  
 low Quality Sequence: trace file contained 24 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Place: LDCM row: A column: 5  
 High quality sequence stop: 10.  
 Location/Qualifiers  
 1. .24  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2819212"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"



REFERENCE 1 (bases 1 to 25)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..25  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD-06-114"  
 /cissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice H1stone Deacetylase overexpression  
 line."

Query Match 0.2%; Score 14.4; DB 1; Length 25;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4016 TGAGATAAAAGAGCAAAACAAA 4039  
 25 TTTAAAAAAGAAAAAAGAAAAA 2

RESULT 1627  
 LOCUS TA388E06P 25 bp DNA linear GSS 13-DEC-2000  
 DEFINITION genomic survey sequence.  
 ACCESSION AL498782  
 VERSION AL498782.1 GI:11874504  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 25)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submision  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. W. Vaubin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
 source  
 1..25  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="388E06"

Query Match 0.2%; Score 14.4; DB 1; Length 25;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6977 AAAACAAACGATGAGGTGGG 7000  
 2 AAAAAAAGAGAGGAGG 25

RESULT 1628  
 LOCUS AZ867155 25 bp DNA linear GSS 21-FEB-2001  
 DEFINITION 2M017F23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0177F23 R, genomic survey sequence.  
 ACCESSION AZ867155  
 VERSION AZ867155.1 GI:13069179  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 Islam, H., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0177 row: F column: 23  
 Seq primer: CACACGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 25.  
 Location/Qualifiers  
 1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0177F23"  
 /sex="Male"  
 /lab\_host="R". Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 25;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4022 AAAAGAGGAAACAAATGTTAT 4045  
Db 1 AAAAAAAAAAAAAAAAAATAATAT 24

#### RESULT 1629

A2348233 25 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0084G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0084G04 R, genomic survey sequence.

ACCESSION A2348233  
VERSION A2348233.1 GI:10427470  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)  
AUTHORS Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0084 row: G column: 04  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

#### FEATURES

##### SOURCE

1. 25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0084G04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 25;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 3382 CTCCTCCCCAGCTGCCACCCCCC 3405  
Db 2 CCCCCCCCCCACCACCCCCC 25

#### RESULT 1630

CF296851/c 26 bp mRNA linear EST 14-AUG-2003  
LOCUS 30DGS--07-G13.B1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
DEFINITION bativa cDNA clone 30DGS--07-G13, mRNA sequence.

ACCESSION CF296851  
VERSION CF296851.1 GI:33665884  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 26)  
AUTHORS Kim, U.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

#### FEATURES

##### SOURCE

1. 26  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultiivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--07-G13"  
/issue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14.4; DB 1; Length 26;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAGAGAGAAAC 4035  
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

#### RESULT 1631

R26779/c 26 bp mRNA linear EST 24-APR-1995  
LOCUS y144f06.s1 Soares placenta Mb2Hp Homo sapiens cDNA clone  
DEFINITION IMAGE:13611 3' similar to gb:W65164 SRPM RESPONSE FACTOR  
ACCESSORY PROTEIN 1A (HUMAN); mRNA sequence.

ACCESSION R26779  
VERSION R26779.1 GI:782914  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 26)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mairra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1384  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LBNL  
 This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert length: 1384 Std Error: 0.00  
 Seq primer: Promega -21m13  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 26  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:538233"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:132611"  
 /sex="Female"  
 /dev\_stage="Placenta obtained at birth (full term)"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares placenta Nb2HP"  
 /note="Organ: placenta; Vector: pTV73D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' AACTGAGAGAAATTCGGCGCGCGAGAAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

Query Match 0.2%; Score 14.4; DB 1; Length 26;  
 Best Local Similarity 75.0%; Freq. No. 2.1e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4016 TGAAGAAAGAGAGAAACAAA 4039  
 Db 24 TTTAAAAAATAAAAAAAAAAAAAA 1

RESULT 1632  
 AZ382581/c 27 bp DNA 1linear GSS 02-OCT-2000  
 LOCUS AZ382581  
 DEFINITION 1M0139120R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 clone UGCGM0139120 R, genomic survey sequence.  
 ACCESSION AZ382581  
 VERSION AZ382581.1 GI:10496281  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuser, A. and Wright, D., Weiss, R.  
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 COMMENT Unpublished (2000)  
 CONTACT Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Place: 0139 row: 1 column: 20  
 Seq primer: CACACAGAAACAGCTATGACC.  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 1. 27  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0139120"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 27;  
 Best Local Similarity 75.0%; Freq. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6977 AAAAACAAGAGAGAGAGTGGG 7000  
 Db 26 AAAAAAAAAAAAAAAAAAGGCGG 3

RESULT 1633  
 TA239G06Q 29 bp DNA 1linear GSS 13-DEC-2000  
 LOCUS TA239G06Q  
 DEFINITION T. brucei sheared genomic DNA clone 239G06, reverse sequence.  
 genomic survey sequence.  
 ACCESSION AL481179  
 VERSION AL481179.1 GI:11846878  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 REFERENCE 1 (bases 1 to 29)  
 AUTHORS Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrel, Oxford University Press, 1999).  
Email: neisayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_t\\_brucei/](http://www.sanger.ac.uk/Projects/T_t_brucei/).

FEATURES  
source  
1..29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="239906"

Query Match  
Best Local Similarity 75.0%; Score 14.4; DB 1; Length 29;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6977 AAAAAACAACAGATGAGTGGG 7000  
|||||  
Db 2 AAAAAAAAAAAAAAAAAAGCGGG 25  
|||||

RESULT 1634  
BX557758/c 29 bp mRNA linear EST 10-OCT-2003  
LOCUS BX557758 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse34e06\_p1c, mRNA sequence.  
ACCESSION BX557758  
VERSION BX557758.1 GI:33428933  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 29)  
Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)

JOURNAL  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
Ranger L157 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all p1c reads are from  
the 3' end.

FEATURES  
source  
1..29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse34e06\_p1c"  
/issue\_type="adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

/db\_xref="taxon:37546"  
/clone="Tse34e06\_p1c"  
/issue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match  
Best Local Similarity 75.0%; Score 14.4; DB 1; Length 29;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4020 AAAAAAGAGAAAACAAATGTT 4043  
|||||  
Db 29 AAAAAAAAAAAAAAAAAACTATT 6  
|||||

RESULT 1635  
BX561329/c 29 bp mRNA linear EST 10-OCT-2003  
LOCUS BX561329 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse55b10\_p1c, mRNA sequence.  
ACCESSION BX561329  
VERSION BX561329.1 GI:33436343  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 29)  
Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)

JOURNAL  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
Ranger L157 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all p1c reads are from  
the 3' end.

FEATURES  
source  
1..29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse55b10\_p1c"  
/issue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"



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RESULT 1636
LOCUS      AL048719
DEFINITION DKF2566G23_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL048719
VERSION     AL048719.1 GI:4727790
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE       EST (Koehrer, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
MIPS        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2566G23"
/cisue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: PAMPI; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 75.0%; Score 14.4; DB 1; Length 33;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy
4016 TCGAAGAAAAAGAGCAAAACAAA 4039
10 TTAACAAAAAATATATATATATATAT 33

RESULT 1637
LOCUS      AL047464
DEFINITION DKF2586M1320_g1 586 (synonym: hutel) Homo sapiens cDNA clone
ACCESSION  AL047464
VERSION     AL047464.1 GI:4727379
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Wambutic, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE       EST (Wambutic, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
MIPS        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

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/clone="DKF2586M1320"
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/clone_lib="586 (synonym: hutel)"
/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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31 AAAAAAAAAAAAAAAAAAAAAAG 8

RESULT 1638
LOCUS      AZ513919/c
DEFINITION IM0360E13F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
ACCESSION  AZ513919
VERSION     AZ513919.1 GI:10695235
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 1000 Std Error: 0.00
            Plate: 0360 row: E column: 13
            Seq primer: CGTTGTAACACGACGCCAGT
            Clases: plasmid ends
            High quality sequence stop: 19.

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/clone_lib="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1|4732114|gb|AF19072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	19	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 1639			
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
Query Match			
Best Local Similarity	84.2%	Pred. Score 14.2; DB 1;	Length 19;
Matches	16;	Conservative	0;
		Mismatches	3;
		Indels	0;
		Gaps	0;

QY	4020	AAAAAGGAGAAACAA	4038	
Db	19	AAAAAAAAAAAAAAAAA	1	
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DEFINITION	AM249916	19 bp	mRNA	linear
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ACCESSION	AM249918			
VERSION	AM249918.1	GI:6592911		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 19)			
AUTHORS	NIH-MGC	http://mgs.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Other ESTs: 2821753..5prime			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgsabbs@remail.nih.gov			
	Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling			
	Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.			
	Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing			
	project Clone distribution: MGC clone distribution information can			
	be found through the I.M.A.G.E. Consortium/LNL, at:			
	www.bio.lnl.gov/bbrp/image/image.html			
	Base Calling / Quality			
	Scores: PHRED from University of Washington Genome Center. Vector			
	Trimming: cross_match from University of Washington Genome Center			
	PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley			
	Drosophila Genome Project. University of Washington Genome Center:			
	http://www.genome.washington.edu			
	Low Quality Sequence: 11			
	contiguous PHRED high quality bases following vector sequence. Very			
	Low Quality Sequence: Trace file contained 19 contiguous distinct			
	peaks following vector sequence. Polyadenylation: Based upon the			
	presence of a XhoI site followed by a run of 14 or more T residues			
	at the beginning of the sequence, this CDNA insert was			
	polyadenylated.			
	Plate: L1CM7	row: K	column: 2	
	High quality sequence stop: 11.			
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	/cell_line="MGC3"			
	/lab_host="DH10B (phage-resistant)"			
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	/note="Organ: lung; Vector: pOTB7. Site 1: XhoI; Site 2:			
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	adapter: GGCAAGAG(G). Size-selected >500bp for average			
	insert size 1.8kb. Library constructed by Ling Hong in			
	the laboratory of Gerald M. Rubin (University of			
	California, Berkeley) using ZAP-CDNA synthesis kit			
	(Stratagene) and Superscript II RT (Life Technologies)."			
Query Match	0.2%	Score 14.2	DB 1	Length 19;
Best Local Similarity	84.2%	Pred. No. 1.5e+03;		
Matches	16;	Conservative 0;	Mismatches 3;	Indels 0;
QY	4474	TTTTTTTTTGTCTTGACA	4492	
Db	1	TTTTTTTTTGTCAACAA	19	
RESULT 1641				
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LOCUS A231628 19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0059M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0059M12 R, genomic survey sequence.  
 ACCESSION A231628  
 VERSION A231628.1 GI:10394503  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 0059 row: M column: 12  
 Seq primer: CACACAGAAACGCTATGACG  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /db\_xref="taxon:10090"  
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 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4034 ACAAAATGTTATTTATA 4052  
 Db 1 ACTAAATTTATTTTAAA 19

RESULT 1642  
 A2357587/c  
 LOCUS AZ357587 19 bp DNA linear GSS 02-OCT-2000

DEFINITION 1M0099C15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0099C15 F, genomic survey sequence.  
 ACCESSION A2357587  
 VERSION A2357587.1 GI:10471287  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 0099 row: C column: 15  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4031 AAAACAAATGTTATTTT 4049  
 Db 19 AAAAAAAAAATTTTTTTT 1

RESULT 1643  
 A2424216/c  
 LOCUS AZ424216 19 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0203011R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION	clone UUGC1M0203011 R, genomic survey sequence.		
VERSION	A2424216		
KEYWORDS	A2424216.1 GI:10548229		
SOURCE	GSS.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
TITLE	Unpublished (2000)		
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0203 row: 0 column: 11 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers		
FEATURES	1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0203011" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_1lb="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	0.2%	Score 14.2;	DB 1; Length 19;
Best Local Similarity	84.2%;	Pred. No. 1.5e+03;	
Matches 16; Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
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Db 19	TTTGTTTGTGTTTGT	1	
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LOCUS	A2447248/c		
DEFINITION	JM0244HH23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244H23 F, genomic survey sequence.		

ACCESSION	AZ447248
VERSION	A2447248.1
KEYWORDS	GI:10599044
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhasen,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5605 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0244 row: H column: 23 Seq primer: CGTTGTAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. 19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0244H23" /sex="male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1 473214 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.2%; Score 14.2; DB 1; Length 19;
Best Local Similarity	84.2%; Pred. No. 1.5e+03;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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A2962226/c	A2962226
LOCUS	2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION	clone UUGC2M0231A02 F, genomic survey sequence.
ACCESSION	A2962226

Location/Qualifiers  
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/notes="Vector: PWD424nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 [g114732114[g]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hanfl,C., Jellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rex,L.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0231 row: P column: 08 Seq primer: CACACAGAAACACTGTGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCM0211P08" /sex="Female" /lab_host="E. coli strain XL10-Gold, TI-resistant, F-" /clone_lbb="Mouse 10kb plasmid UUGCM library" /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.2%; Score 14.2; DB 1; Length 19;
Best Local Similarity	84.2%; Pid. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Oy	3617 GGATGGCGTGTGGGCTGG 3635
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LOCUS	AZ486787/c
DEFINITION	IM0315D23F Mouse 10kb plasmid UUGCM library Mus musculus genomic
ACCESSION	c1one UUGCM0315D23 F. genomic survey sequence.
VERSION	AZ486787
KEYWORDS	AS. GI:106533904
GSS.	

**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 20)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0315 row: D column: 23  
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 Class: plasmid ends  
 High quality sequence stop: 20.  
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 /clone\_lib="Mouse 10kb plasmid UUCIM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gblAf129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORGANISM** Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 20)  
**AUTHORS** Kim, V.S., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
**FEATURES**  
**SOURCE**  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site 1: Sati; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with Sati and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

**Query Match** 0.2%; Score 14.2; DB 1; Length 20;  
**Best Local Similarity** 84.2%; Pred. No. 1.6e+03;  
**Matches** 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**RESULT 1649**  
**LOCUS** AU267884 20 bp mRNA linear EST 10-MAY-2002  
**DEFINITION** AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA sequence.  
**ACCESSION** AU267884  
**VERSION** AU267884.1 GI:20526682  
**KEYWORDS** EST.  
**SOURCE** Dictyostelium discoideum  
**ORGANISM** Dictyostelium discoideum  
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
**REFERENCE** 1 (bases 1 to 20)  
**AUTHORS** Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.  
**TITLE** Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Hideko Urushihara  
 Institute of Biological Sciences  
 University of Tsukuba  
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
 Tel: 81-298-53-4664  
 Fax: 81-298-53-6614  
 Email: hideko@biol.tsukuba.ac.jp.  
**FEATURES**  
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 /strain="AX4"  
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4469 TTTTGTCTTTTGTCT 4487  
Db 2 TTTTGTCTTTTCTCT 20

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AUS267884/c

LOCUS AUS267884 20 bp mRNA linear EST 10-MAY-2002  
DEFINITION AUS267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA  
sequence.

ACCESSION AUS267884  
VERSION AUS267884.1 GI:20526682  
KEYWORDS EST.

SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

REFERENCE 1 (bases 1 to 20)  
Unruhshara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,  
Takeuchi, I., Kohara, Y., and Tanaka, Y.

TITLE Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
Unpublished (2002)

JOURNAL Contact: Hideko Unruhshara  
Institute of Biological Sciences

University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@bio1.tsukuba.ac.jp.

FEATURES  
source Location/Qualifiers

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Qy 4017 GAGAAAAAGAGAAAC 4035  
Db 19 GAGAAAAAGCAAAAAC 1

RESULT 1651

LOCUS B0586354 20 bp mRNA linear EST 06-DEC-2002  
DEFINITION B0586354 E01395-024-013-F10-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-013-F10 5-PRIME, mRNA sequence.

ACCESSION B0586354  
VERSION B0586354.1 GI:26115926  
KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 20)  
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mp1z-koeln.mpg.de  
Insert Length: 20 Std Error: 0.00  
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Seq primer: Sp6; CATACGATTTCGACACTATAG.

FEATURES  
source Location/Qualifiers

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/note="Vector: PCWVS-PORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polya-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3373 TTTTGTCTCTCTCTCC 3391  
Db 2 TTTGTCTCTCTCTCTCC 20

RESULT 1652

LOCUS C53693 20 bp mRNA linear EST 11-SEP-1997  
DEFINITION C53693 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA  
clone YK323c3 3', mRNA sequence.

ACCESSION C53693  
VERSION C53693.1 GI:2391450  
KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Pelodetidae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 20)  
Kohara, Y., Mochizuki, T., Tabara, H., Watanabe, H., Sugimoto, A.,  
Sano, M., Miyata, A. and Nishigaki, A.  
Expression map of the C.elegans genome  
Unpublished (1996)  
Contact: Yuji Kohara  
Genome Biology Lab.  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.

FEATURES  
Location/Qualifiers

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Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      6234 GCACTGTTCTTGATGTT 6252
Db      19 GCGCTGTTCTTCTGTT 1

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DEFINITION      IM0553B1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC1M0553B1 F, genomic survey sequence.
ACCESSION      AZ759903
VERSION        AZ759903.1 GI:12867167
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: B column: 11
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

```

10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      6778 CTTTACTATTGGCCTT 6796
Db      19 CTTTACAGTTTGCTT 1

RESULT 1654
LOCUS      AZ827842      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION      2M0104F03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC2M0104F03 R, genomic survey sequence.
ACCESSION      AZ827842
VERSION        AZ827842.1 GI:12997750
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 20.
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```



electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7395 TTCTGAAGCAGACATC 7413  
DB 1 TTCTGTGCAAGAAACATC 19

RESULT 1655  
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LOCUS 2M0129008F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0129008 F, genomic survey sequence.  
ACCESSION A2835133  
VERSION A2835133.1 GI:13005041  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
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High quality sequence stop: 20.  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB 2 TTTTGTGTAAGATA 20

RESULT 1656  
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LOCUS 2M0129008F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0129008 F, genomic survey sequence.  
ACCESSION A2835133  
VERSION A2835133.1 GI:13005041  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0129 row: O column: 08  
Seq primer: CGTTGTAACAGCAGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number



purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4021 AAAAGAGAAACAAA 4039  
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RESULT 1659

AZ346714/c

LOCUS AZ346714 21 bp DNA linear GSS 29-SEP-2000

DEFINITION IM0082N05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ346714 clone UGCG1M0082N05 F, genomic survey sequence.

VERSION AZ346714.1 GI:10425951

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baes 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0082 row: N column: 05  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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FEATURES

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/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 1660

AZ399828/c

LOCUS AZ399828 21 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0165A23R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ399828 clone UGCG1M0165A23 R, genomic survey sequence.

VERSION AZ399828.1 GI:10514902

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baes 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0165 row: A column: 23  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21

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/organism="Mus musculus"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2999 CCCCACCCCTGACCCCATC 3017  
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RESULT 1661  
AZ475883/c

LOCUS 21 bp DNA linear GSS 04-OCT-2000  
DEFINITION JMC294J14F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION AZ475883  
VERSION AZ475883.1 GI:10634008

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Seq primer: CGTGTAAACGACGCCAGCT

Class: plasmid ends  
High quality sequence stop: 21.

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/mol\_type="genomic DNA"  
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/clone="UUCG1M0294J14"  
/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1[4732114]gb[AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5704 CTTCCCTTTCCTCTCTCT 5722  
19 CTTCTTTCCTCCCTCTCT 1

RESULT 1662  
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LOCUS 21 bp DNA linear GSS 14-DEC-2000  
DEFINITION JMC294J14F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION AZ654730  
VERSION AZ654730.1 GI:11791876

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: P column: 05  
Seq primer: CGTGTAAACGACGCCAGCT

Class: plasmid ends  
High quality sequence stop: 21.

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1[4732114]gb[AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
 Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGGTGGAGAGG 3640  
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 Db 20 GGGGTGGGGATGGGTAAAG 2

RESULT 1663  
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 LOCUS AZ774703  
 DEFINITION 2M0004G14F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGM0004G14 F, genomic survey sequence.  
 ACCESSION AZ774703  
 VERSION AZ774703.1 GI:1290261  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0004 row: G column: 14  
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 Class: plasmid ends  
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 Location/Qualifiers

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 /clone="UGCGM0004G14"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
 Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGGTGGAGAGG 3640  
 |||||  
 Db 20 GGGGGGGGGGTGGGGGGG 2

RESULT 1664  
 AZ809249 21 bp DNA linear GSS 20-FEB-2001  
 LOCUS AZ809249  
 DEFINITION 2M0073112F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGM0073112 F, genomic survey sequence.  
 ACCESSION AZ809249  
 VERSION AZ809249.1 GI:12975387  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0073 row: I column: 12  
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 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match

0.2%; Score 14.2; DB 1; Length 21;

Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4467 TTTTGTGTGTGTGTGT 4485  
Db 2 TTTGTGTGTGTGTGTGT 20

## RESULT 1665

AZ936997 21 bp DNA linear GSS 26-APR-2001  
LOCUS AZ936997  
DEFINITION 2M0195H01F Mouse 10kb plasmid UGCC2M library Mus musculus genomic  
clone UGCC2M0195H01 F, genomic survey sequence.

ACCESSION AZ936997  
VERSION AZ936997.1 GI:13795578  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

FEATURES  
source  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0195 row: H column: 01  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1..21

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/clone\_lib="Mouse 10kb plasmid UGCC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passages through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 [g1|4732114|9b|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 774 CCACCCGCTGGGGGCTGGG 792  
Db 2 CTTCCCTGGGGGCTGGG 20

## RESULT 1666

CF313297 23 bp mRNA linear EST 15-AUG-2003  
LOCUS CF313297/c  
DEFINITION HD-01-G01.G1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD-01-G01, mRNA sequence.

ACCESSION CF313297  
VERSION CF313297.1 GI:33685058  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers

FEATURES  
source  
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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E. coli DH10B"  
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/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.2%; Score 14.2; DB 1; Length 23;  
Best Local Similarity 84.2%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 20 AAAAAAGAAAAA 2

## RESULT 1667

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LOCUS AZ984045/c  
DEFINITION 2M0265I23F Mouse 10kb plasmid UGCC2M library Mus musculus genomic  
clone UGCC2M0265I23 F, genomic survey sequence.

ACCESSION AZ984045  
VERSION AZ984045.1 GI:13855272  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
64112, USA  
Tel: 801 585 5606  
Fax: 801 585 5177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Date: 0000-00-00

Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends

FEATURES	Location/Qualifiers
source	1. .23

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/clone_1ib="Mouse 10kb plasmid UUCGCM library"
/notes="Vector: PWD24nv. Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
pMD242 [gsl473214|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorised mouse DNA was annealed to
adaptorised vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match	0.2%	Score 14.2	DB 1	length 23
Best Local Similarity	84.2%	Pred. No. 2e+03		
Matches 16	Conservative	0	Mismatches 3	Indels 0
QY	3984	TGCTCTATACAAAAAACT	4002	
Db	22	TGCTCTAAAAAAAAT	4	

RESULT	1668					
AZ399663/c						
LOCUS	AZ399663	24 bp	DNA	linear	GSS	03-OCT-2000
DEFINITION	M0165C10 Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0165C10 R, genomic survey sequence.					
ACCESSION	AZ399663					
VERSION	AZ399663.1	GI:10514737				
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)					
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,					

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	Unpublished (2000)
COMMENT	plasmid inserts Contact: Robert B. Weiss Institute of Virology, University of Utah, Salt Lake City, UT 84143

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert length: 10000 Std Error: 0.000  
Plate: 0165 row: C column: 10  
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 24.

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source
1. .24
/organism="Mus musc
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/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGClM0165C10"  
 /sex="Male"  
 /lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGClM library"  
 /note="Vector: PMW42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repigated with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 sheared DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMW42 [g11432114|g1b|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent B. coli XL10-gold (Stratagene) cells  
 and selected for ampicillin resistance."

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGClM0165C10"  
 /sex="Male"  
 /lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGClM library"  
 /note="Vector: PGM4247v; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repated with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 sheared DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [g11432114|9b|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent *E. coli* XL10-gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match	0.24;	Score 14.2;	DB 1;	Length 24;
Best Local Similarity	84.24;	Pred. No. 2.1e+03;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Cy	4022	AAAAGACGAAACAAAT	4040	
Db	23	AAAAAAAAAAAACAAAT	5	

RESULT	1669
CF328811/c	
LOCUS	CF328811 27 bp mRNA linear EST 18-AUG-2003
DEFINITION	NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION	sativa cDNA clone NACL--03-009, mRNA sequence.
VERSION	CF328811
KEYWORDS	CF328811.1 GI:33605864
SOURCE	EST.
ORGANISM	Oryza sativa
	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Erbartoideae; Oryzaceae; Oryza.
	1 (bases 1 to 27)
REFERENCE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS	Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

1..27  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--03-009"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2M6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14.2; DB 1; Length 27;  
Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAACAA 4038  
Db 27 AAAAAAAAAATTAATAAAAAAAAA 1

RESULT 1670  
T165H05P/c 27 bp DNA linear GSS 13-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 165h05, forward sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AL472045  
VERSION AL472045.1 GI:11837399  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 27)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Email: nelesyde@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source

1..27  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="165h05"

Query Match 0.2%; Score 14.2; DB 1; Length 27;  
Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4032 AACCAAAATGTAATTTATACATTA 4058  
Db 27 AAAAAAAAACTTTTAAAAAAAAAAAA 1

RESULT 1671  
CE277114/c 28 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ETL--02-111.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
DEFINITION Oryza sativa cDNA clone 14ETL--02-111, mRNA sequence.  
ACCESSION CE277114  
VERSION CE277114.1 GI:33654500  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriatroidae; Oryzaceae; Oryza.  
1 (bases 1 to 28)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

REFERENCE  
AUTHORS Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

1..28  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--02-111"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14.2; DB 1; Length 28;  
Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4021 AAAAAAGAGAAAAAANA 4039  
Db 21 AAAAAAGAAAAAAAAAAAAA 3

RESULT 1672  
BX554068/c 31 bp mRNA linear EST 10-OCT-2003  
LOCUS BX554068 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse13c01\_pic, mRNA sequence.  
ACCESSION BX554068  
VERSION BX554068.1 GI:33378169  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hypoboscidae; Glossinidae; Glossina.



REFERENCE 1 (bases 1 to 31)  
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..31  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse32f01\_pic"  
 /issue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4021 AAAAGAGAGAAACAAATGTTATT 4047  
 |||||  
 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1673  
 BXS57470/c 31 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BXS57470 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse32f01\_pic, mRNA sequence.  
 ACCESSION BXS57470  
 VERSION BXS57470.1 GI:33428655  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.  
 1 (bases 1 to 31)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
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 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,

REFERENCE 1 (bases 1 to 31)  
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..31  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse32f01\_pic"  
 /issue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4021 AAAAGAGAGAAACAAATGTTATT 4047  
 |||||  
 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1674  
 BXS58479/c 31 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BXS58479 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse38n04\_pic, mRNA sequence.  
 ACCESSION BXS58479  
 VERSION BXS58479.1 GI:33365232  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.  
 1 (bases 1 to 31)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..31  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse38n04\_pic"  
 /issue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4021 AAAAAGAGAAAACAAATGTTATTT 4047  
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1675  
 EX559254/c 31 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX559254 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse42e03\_p1c, mRNA sequence.  
 ACCESSION BX559254  
 VERSION BX559254.1 GI:33366605  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 31)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

REFERENCE  
 AUTHORS 1 (bases 1 to 31)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

TITLE  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..31  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:37546"  
 /clone="Tse42e03\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4021 AAAAAGAGAAAACAAATGTTATTT 4047  
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1676  
 BX551100 32 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX551100 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse116f01\_p1c, mRNA sequence.  
 ACCESSION BX551100  
 VERSION BX551100.1 GI:33374951  
 KEYWORDS EST.

SOURCE  
 ORGANISM Glossina morsitans morsitans  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 32)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

REFERENCE  
 AUTHORS 1 (bases 1 to 32)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

TITLE  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..32  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse116f01\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 32;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4021 AAAAAGAGAAAACAAATGTTATTT 4047  
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1677  
 BX553142/c 33 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX553142 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse127f01\_p1c, mRNA sequence.  
 ACCESSION BX553142  
 VERSION BX553142.1 GI:33377335  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 33)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

REFERENCE  
 AUTHORS 1 (bases 1 to 33)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

TITLE  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.

FEATURES  
 source Location/Qualifiers  
 1..33  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse127f01\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 32;  
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4021 AAAAAGAGAAAACAAATGTTATTT 4047  
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1678  
 BX551100 32 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX551100 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse116f01\_p1c, mRNA sequence.  
 ACCESSION BX551100  
 VERSION BX551100.1 GI:33374951  
 KEYWORDS EST.

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/lab_host="EMDH10B"
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/note=Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Bindeck, Germany; contact:  
b.schulz@kws.de; Cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

## RESULT 1680

BQ587890

LOCUS BQ587890 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION S013302-024-009-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-009-B02 3-PRIME, mRNA sequence.

ACCESSION BQ587890  
VERSION BQ587890.1 GI:26117472  
KEYWORDS EST.

## SOURCE

ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS

Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

## TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
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Fax: 00492215062851  
Email: weishaar@mp1z-koeln.mpg.de  
Insert length: 14 Std Error: 0.00  
Plate: 9 row: B column: 02  
Seq primer: T7; GTATACGACTCATTATGAGGC.  
Location/Qualifiers

## FEATURES

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Kleinwanzlebener Saatzzucht AG Bindeck, Germany; contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

## RESULT 1681

BQ589191

LOCUS BQ589191 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION S014009-024-015-120-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-015-120 3-PRIME, mRNA sequence.

ACCESSION BQ589191  
VERSION BQ589191.1 GI:26118774  
KEYWORDS EST.

## SOURCE

ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS

Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

## TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weishaar B  
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Fax: 00492215062851  
Email: weishaar@mp1z-koeln.mpg.de  
Insert length: 14 Std Error: 0.00  
Plate: 15 row: I column: 20  
Seq primer: T7; GTATACGACTCATTATGAGGC.  
Location/Qualifiers

## FEATURES

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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Bindeck, Germany; contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;  
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Qy 4464 TTTT TTTT TTTT TTTT 4477  
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RESULT 1682  
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 DEFINITION E012840-024-019-E16-SP6 MP12-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0590242  
 VERSION B0590242  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 14)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weisshaar B  
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 Fax: 00492215062851  
 Email: weisshaar@mplz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 19 row: E column: 16  
 Seq primer: SP6; CATACGATTAGTCACTATAG.  
 Location/Qualifiers  
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 /cissue\_type="storage root"  
 /lab\_host="EMDH10B"  
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14; DB 1; Length 14;  
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1683  
 LOCUS B0590261 14 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012844-024-019-K14-T7 MP12-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0590261  
 VERSION B0590261  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 14)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weisshaar B  
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 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mplz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
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 Seq primer: T7; GTAATACGACTCATATAGCG.  
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
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QY 4464 TTTT TTTT TTTT TTTT 4477  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1684  
 LOCUS B0591168 14 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012715-024-017-H18-T7 MP12-ADIS-024-storage root Beta vulgaris  
 ACCESSION B0591168  
 VERSION B0591168  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 14)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 COMMENT Contact: Weisshaar B  
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 Fax: 00492215062851  
 Email: weisshaar@mplz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 19 row: K column: 14  
 Seq primer: T7; GTAATACGACTCATATAGCG.  
 Location/Qualifiers  
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

MEDLINE  
12472698  
PUBMED

COMMENT  
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Fax: 00492215062851  
Email: weishnae@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00  
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FEATURES  
source

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/lab\_host="EMDH10B"

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/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinanwaldbener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:

SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4477  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1685  
BOS91176

LOCUS BOS91176 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012715-024-017-N20-T7 MPiZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-N20 3-PRIME, mRNA sequence.

ACCESSION BOS91176  
VERSION BOS91176.1 GI:26120759

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)  
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

REFERENCE

AUTHORS

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Insert Length: 14 Std Error: 0.00

Plate: 17 row: N column: 20

JOURNAL

MEDLINE

PUBMED

COMMENT

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Email: weishnae@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 17 row: N column: 20

FEATURES  
source

Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
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cDNA library from sugar beet, library provided by KWS  
Kleinanwaldbener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:

SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4477  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1686  
BOS91207

LOCUS BOS91207 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012715-024-017-B04-T7 MPiZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-B04 3-PRIME, mRNA sequence.

ACCESSION BOS91207  
VERSION BOS91207.1 GI:26120790

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)  
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

REFERENCE

AUTHORS

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Insert Length: 14 Std Error: 0.00

Plate: 17 row: B column: 04

JOURNAL

MEDLINE

PUBMED

COMMENT

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Fax: 00492215062851

Email: weishnae@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 17 row: B column: 04

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-Notti, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-Notti-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTT 4477  
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Db 1 TTTTTTTTTTTT 14

RESULT 1687  
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LOCUS E012713-024-017-B15-17 MP1Z-ADIS-024-storage root Beta vulgaris  
DEFINITION cDNA clone 024-017-B15 3-PRIME, mRNA sequence.  
ACCESSION BOS91380  
VERSION BOS91380.1 GI:26121063  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
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Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
ADIS DNA core facility at MP1Z  
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Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 17 row: B column: 15  
Seq primer: T7; GTAATACGACCTCACTATAGGCG.  
Location/Qualifiers  
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orientation:  
SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-Notti-T7; Note:  
Sequencing granted in the context of the GABI-Beet

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b.schulz@kws.de; cloning sites Sali-Notti, primer sites and  
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Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;  
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RESULT 1688  
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DEFINITION cDNA clone 024-017-M04 3-PRIME, mRNA sequence.  
ACCESSION BOS91482  
VERSION BOS91482.1 GI:26121065  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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b.schulz@kws.de; cloning sites Sali-Notti, primer sites and  
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Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

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b.schulz@kws.de; cloning sites Sali-Notti, primer sites and  
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SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-Notti-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Db 1 TTTTTTTTTTTT 14

RESULT 1689

LOCUS B0593052 14 bp mRNA linear EST 06-DEC-2002

DEFINITION E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris

ACCESSION B0593052

VERSION B0593052.1 GI:26122635

KEYWORDS EST.

ORGANISM Beta vulgaris

SOURCE Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

REFERENCE 1 (bases 1 to 14)

1 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weishaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

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SP6-Sali-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZP/GABI-Primary database: <http://gabi.rzp.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTTTTTTTTTT 14

Db 1 TTTTTTTTTTTT 14

RESULT 1690

LOCUS CF277935 14 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF277935

VERSION CF277935.1 GI:33655321

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

1 (bases 1 to 14)

1 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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1 TTTTTTTTTTTT 14

Db 1 TTTTTTTTTTTT 14

RESULT 1691

LOCUS CF278001 14 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF278001

VERSION CF278001.1 GI:33655387

KEYWORDS EST.

ORGANISM Oryza sativa

SOURCE Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

1 (bases 1 to 14)

1 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1692  
 CF278452

LOCUS CF278452 14 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 ORYZA sativa cDNA clone 14ETL--04-F22, mRNA sequence.

ACCESSION CF278452  
 VERSION CF278452.1 GI:33655838  
 KEYWORDS EST.

ORGANISM Oryza sativa  
 SOURCE Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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RESULT 1693  
 CF279473 14 bp mRNA linear EST 14-AUG-2003  
 LOCUS CF279473

DEFINITION 14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 ORYZA sativa cDNA clone 14ETL--05-M14, mRNA sequence.

ACCESSION CF279473  
 VERSION CF279473.1 GI:33656859  
 KEYWORDS EST.

ORGANISM Oryza sativa  
 SOURCE Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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RESULT 1694  
 CF279992

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 DEFINITION 14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
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ACCESSION CF279992  
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ORGANISM Oryza sativa  
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REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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Db

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LOCUS      14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION      Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION      CF281958
VERSION      CF281958.1 GI:33659345
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Db

TITLE      JOURNAL
COMMENT

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RESULT 1696
CF282350      14 bp mRNA linear EST 14-AUG-2003
LOCUS      14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION      Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION      CF282350
VERSION      CF282350.1 GI:33659737
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Db

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LOCUS      30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION      sativa cDNA clone 30DGS--03-P15, mRNA sequence.
ACCESSION      CF294449
VERSION      CF294449.1 GI:33663482
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.  
 Location/Qualifiers

## FEATURES

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1. 14  
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## RESULT 1698

CF295570

LOCUS 14 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 30DS--05-J06.g1 Rice leaf plasmid cDNA library I (30DS) Oryza  
 ACCESSION CF295570  
 VERSION CF295570.1 GI:33664603  
 KEYWORDS EST.

## SOURCE

Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.  
 Location/Qualifiers

## REFERENCE

AUTHORS

## TITLE

JOURNAL

## COMMENT

## FEATURES

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1. 14  
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DB 1 TTTT TTTT TTTT TTTT 14

## RESULT 1699

CF296120

LOCUS 14 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 30DS--06-F17.b1 Rice leaf plasmid cDNA library I (30DS) Oryza  
 ACCESSION CF296120  
 VERSION CF296120.1 GI:33665153  
 KEYWORDS EST.

## SOURCE

Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.  
 Location/Qualifiers

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Query Match 0.2%; Score 14; DB 1; Length 14;  
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Oy 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT 14

## RESULT 1700

CF297969

LOCUS 14 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 ACCESSION CF297969  
 VERSION CF297969.1 GI:33669730  
 KEYWORDS EST.

## SOURCE

Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Bioinformatics, Myongji University

Query Match 0.2%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477  
 |||||

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Tel: 82 31 330 6193  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

## SOURCE

1. .14  
/organism="Oryza sativa"  
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QY 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

Db

# RESULT 1701

CF298109 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--01-F19, mRNA sequence.  
ACCESSION CP298109  
VERSION CP298109.1 GI:33669870  
KEYWORDS EST.

# ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriactoidae; Oryzaceae; Oryza.

# REFERENCE

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

# COMMENT

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

## SOURCE

1. .14  
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/mol\_type="mRNA"  
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QY 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

# RESULT 1702

CF299368 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--03-F21, mRNA sequence.  
ACCESSION CP299368  
VERSION CP299368.1 GI:33671129  
KEYWORDS EST.

# ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriactoidae; Oryzaceae; Oryza.

# REFERENCE

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

# COMMENT

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

## SOURCE

1. .14  
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QY 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

Db

# RESULT 1703

CF300542 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--05-B01, mRNA sequence.  
ACCESSION CF300542  
VERSION CF300542.1 GI:33672303  
KEYWORDS EST.

# ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriactoidae; Oryzaceae; Oryza.

# REFERENCE

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

# COMMENT

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Location/Qualifiers

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RESULT 1704  
CF301020 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--05-L10, mRNA sequence.  
ACCESSION CF301020  
VERSION CF301020.1 GI:33672781  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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Location/Qualifiers

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RESULT 1705

CF301083 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--05-M19, mRNA sequence.  
ACCESSION CF301083  
VERSION CF301083.1 GI:33672844  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .14  
Location/Qualifiers

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RESULT 1706

CF301380 14 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--06-D16, mRNA sequence.  
ACCESSION CF301380  
VERSION CF301380.1 GI:33673141  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
SOURCE  
1. .14  
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RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;  
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Oy 4464 TTTT TTTT TTTT TTTT 4477  
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## RESULT 1707

CF302675

LOCUS 7LEAF--08-G18 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--08-G18, mRNA sequence.  
ACCESSION CF302675  
VERSION CF302675.1 GI:33674436  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
SOURCE  
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RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477  
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## RESULT 1708

CF302846

LOCUS 7LEAF--08-M05 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--08-M05, mRNA sequence.  
ACCESSION CF302846  
VERSION CF302846.1 GI:33674607  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1709  
CF308006  
LOCUS ABF--01-K10 g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.  
ACCESSION CF308006  
VERSION CF308006.1 GI:33679767  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## COMMENT

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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1.14
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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO, Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1710

## LOCUS

CF308220 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.

ACCESSION CF308220  
VERSION CF308220.1 GI:33679981

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

## TITLE

## JOURNAL

## COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1711

## LOCUS

CF308445 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.

ACCESSION CF308445  
VERSION CF308445.1 GI:33680206

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

## TITLE

## JOURNAL

## COMMENT

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO, Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1712

## LOCUS

CF308918 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.

## ACCESSION

## VERSION

CF308918  
CF308918.1 GI:33680679

## KEYWORDS

## EST.

SOURCE  
ORGANISM Oryza sativa

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT 14

RESULT 1713  
CF310714 14 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--05-111.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-111, mRNA sequence.  
ACCESSION CF310714  
VERSION CF310714.1 GI:33682475  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euhartoidae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
SOURCE 1..14  
/organism="Oryza sativa"  
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Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT 14

RESULT 1714  
CF311201 14 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.  
ACCESSION CF311201  
VERSION CF311201.1 GI:33682962  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euhartoidae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
SOURCE 1..14  
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/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
CDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT 14



RESULT 1715

CF311813

LOCUS CF311813 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.

ACCESSION CF311813

VERSION CF311813.1 GI:33563574

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol\_type="mRNA"

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/db\_xref="taxon:4530"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO, Site\_1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 1716

CF318323

LOCUS CF318323 14 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.

ACCESSION CF318323

VERSION CF318323.1 GI:33690084

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--08-G13"

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/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 1717

CF318450

LOCUS CF318450 14 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--08-J08.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.

ACCESSION CF318450

VERSION CF318450.1 GI:33690211

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--08-J08"

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/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

## RESULT 1718

CF319826 14 bp mRNA linear EST 15-AUG-2003  
LOCUS HD-10-H16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD-10-H16, mRNA sequence.  
ACCESSION CF319826  
VERSION CF319826.1 GI:33691587  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
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Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

## RESULT 1719

CF321246 14 bp mRNA linear EST 15-AUG-2003  
LOCUS HD-12-G24.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD-12-G24, mRNA sequence.  
ACCESSION CF321246  
VERSION CF321246.1 GI:33693007  
KEYWORDS EST.  
SOURCE Oryza sativa

FEATURES  
SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/tissue\_type="callus"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
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Fax: 82 31 321 6355  
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.

FEATURES  
SOURCE location/Qualifiers  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

RESULT 1720 14 bp mRNA linear EST 18-AUG-2003  
CF327097  
LOCUS NACL-01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL-01-H01, mRNA sequence.  
ACCESSION CF327097  
VERSION CF327097.1 GI:33802449  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
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Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.

FEATURES  
SOURCE location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="Nackdong"

FEATURES  
SOURCE

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Query Match 0.2%; Score 14; DB 1; Length 14;  
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QY 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT TTTT 14

## RESULT 1721

CF327119

LOCUS CF327119 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--01-H14, mRNA sequence.

ACCESSION CF327119

VERSION CF327119.1 GI:33802493

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

JOURNAL

COMMENT

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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

## FEATURES

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 1 TTTT TTTT TTTT TTTT 14

## RESULT 1722

CF327203

LOCUS CF327203 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--01-J16, mRNA sequence.

ACCESSION CF327203  
 VERSION CF327203.1 GI:33802665  
 KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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 Unpublished (2003)

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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

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## RESULT 1723

CF327445

LOCUS CF327445 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--01-O24, mRNA sequence.

ACCESSION CF327445

VERSION CF327445.1 GI:33803149

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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 Unpublished (2003)

JOURNAL

COMMENT

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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

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 1 TTTT TTTT TTTT TTTT 14

## RESULT 1724

LOCUS CF328490 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--03-G21, mRNA sequence.

ACCESSION CF328490  
 VERSION CF328490.1 GI:33805226  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.

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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

SOURCE

1..14  
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Query Match 0.2%; Score 14; DB 1; Length 14;  
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OY 4464 TTTT TTTT TTTT TTTT 4477  
 |||||  
 1 TTTT TTTT TTTT TTTT 14

## RESULT 1725

LOCUS CF328540 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--03-H24, mRNA sequence.

ACCESSION CF328540  
 VERSION CF328540.1 GI:33805324  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.

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Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

SOURCE

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OY 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT TTTT 14

## RESULT 1726

LOCUS CF328669 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--03-K23, mRNA sequence.

ACCESSION CF328669  
 VERSION CF328669.1 GI:33805587  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.

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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

SOURCE

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

RESULT 1727  
LOCUS CF328994 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza  
ACCESSION CF328994  
VERSION CF328994.1 GI:33806228  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Oryza sativa  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

RESULT 1728  
LOCUS CF329217 14 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-H10, mRNA sequence.

ACCESSION CF329217  
VERSION CF329217.1 GI:33806672  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Oryza sativa  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

CONTACT: Nahm B.H.  
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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1729  
LOCUS CF329990/c 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--05-111.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-111, mRNA sequence.

ACCESSION CF329990  
VERSION CF329990.1 GI:33808202  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Oryza sativa  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

CONTACT: Nahm B.H.  
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Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

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/organism="Oryza sativa"
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/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Qy 4464 TTTT TTTT TTTT TTTT 4477  
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RESULT 1730  
 CF330784 14 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--06-K10, mRNA sequence.

ACCESSION CF330784  
 VERSION CF330784.1 GI:33809790  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE JOURNAL  
 COMMENT Contact: Nahm B.H.  
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 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
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 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
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RT-PCR."

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Qy 4464 TTTT TTTT TTTT TTTT 4477  
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 Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1731  
 CF331272

LOCUS CF331272 14 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--07-F09, mRNA sequence.

ACCESSION CF331272  
 VERSION CF331272.1 GI:33810755  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE JOURNAL  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Qy 4464 TTTT TTTT TTTT TTTT 4477  
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 Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1732  
 CF331861 14 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--08-C10, mRNA sequence.

ACCESSION CF331861  
 VERSION CF331861.1 GI:33811945  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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 Unpublished (2003)

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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1733
CF333214 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-A10.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333214
VERSION CF333214.1 GI:33814707
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES
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Oy 4464 TTTT TTTT TTTT TTTT 4477
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1733
CF333215/c 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-A10.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333215
VERSION CF333215.1 GI:33814709
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/notes="Vector: PCR-TOP0; Site 1: EcoRI; Oligo-capped mRNA
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Query Match
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1735
CF333399 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-B12.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-B12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
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Db 1 TTTT TTTT TTTT TTTT 14

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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1735
CF333399 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-B12.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-B12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

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prepared from Arabidopsis Jasmonate Carboxyl
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OY 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1736

CF334202

LOCUS

DEFINITION JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.

ACCESSION

CF334202

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1737

CF334281

LOCUS

DEFINITION JMT--03-105.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--03-105, mRNA sequence.

ACCESSION

CF334281

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 1738

CF334290

LOCUS

DEFINITION JMT--03-111.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--03-111, mRNA sequence.

ACCESSION

CF334290

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.  
1 (bases 1 to 14)

REFERENCE



**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
**TITLE** Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**JOURNAL** Large-scale Sequencing Analysis of Rice ESTs  
**COMMENT** Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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**Qy** 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT 14

## RESULT 1739

**LOCUS** CF335781 14 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** JMT--05-J13.b1 AtUMT-overexpressing transgenic rice plasmid cDNA  
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**ACCESSION** CF335781  
**VERSION** CF335781.1 GI:33819936  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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**Qy** 4464 TTTT TTTT TTTT TTTT 4477  
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**RESULT 1740**  
**LOCUS** CF336094 14 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** JMT--06-A10.G1 AtUMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.  
**ACCESSION** CF336094  
**VERSION** CF336094.1 GI:33820566  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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**Query Match**  
 Best Local Similarity 100.0%; DB 1; Length 14;  
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**Qy** 4464 TTTT TTTT TTTT TTTT 4477  
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 1 TTTT TTTT TTTT 14

**RESULT 1741**  
**LOCUS** CF336106 14 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** JMT--06-A17.b1 AtUMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.  
**ACCESSION** CF336106  
**VERSION** CF336106.1 GI:33820590

KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
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/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1742  
CF336287 14 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.  
ACCESSION CF336287  
VERSION CF336287.1 GI:33820962  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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1 TTTT TTTT TTTT TTTT 14

RESULT 1743  
CF336906 14 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.

ACCESSION CF336906  
VERSION CF336906.1 GI:33822182  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 0.2%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1744  
CF295100 15 bp mRNA linear EST 14-AUG-2003  
LOCUS 30DS--04-002.b1 Rice leaf plasmid cDNA library I (30DS) Oryza  
DEFINITION Bativa cDNA clone 30DS--04-002, mRNA sequence.  
ACCESSION CF295100  
VERSION CF295100.1 GI:33664133  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
|||||  
Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1745  
CF329379 15 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION Bativa cDNA clone NACL--04-K23, mRNA sequence.  
ACCESSION CF329379  
VERSION CF329379.1 GI:33806995  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

FEATURES  
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/clone="NACL--04-K23"  
/issue\_type="callus"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
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Db 16 TTTT TTTT TTTT TTTT 3

RESULT 1746  
CF291803 16 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION Bativa cDNA clone 14ROOT--02-G05, mRNA sequence.  
ACCESSION CF291803  
VERSION CF291803.1 GI:33660836  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TTTT TTTT TTTT TTTT 3

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RESULT 1747
AM250784      17 bp      mRNA      linear      EST 07-JAN-2000
LOCUS         2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3',
DEFINITION    mRNA sequence.
ACCESSION     AM250784
VERSION       AM250784.1 GI:6593777
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE         NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
               Other ESTs: 2822335.5prime
               Contact: Robert Strausberg, Ph.D.
               Email: cgaabs-remail.nih.gov
               Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
               Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
               Consortium (ULNL) DNA Sequencing by: Berkeley MGC sequencing
               project clone distribution: MGC clone distribution information can
               be found through the I.M.A.G.E. Consortium/ULNL at:
               www-bio.llnl.gov/bdrp/image/image.html Base Calling / Quality
               Trimming: cross match from University of Washington Genome Center
               PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
               Drosophila Genome Project. University of Washington Genome Center:
               http://www.genome.washington.edu low Quality Sequence: 0 contiguous
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               following vector sequence.
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               Location/Qualifiers
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               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH_MGC 7"
               /note="Organ: lung; Vector: pGB7; Site_1: XhoI; Site_2:
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               adaptor: GGCACGAG(G). Size-selected >500bp for average
               insert size 1.8kb. Library constructed by Ling Hong in
               the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.2%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 TTNNTTTT TTTT TTTT 17
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RESULT 1748
CF339347      17 bp      mRNA      linear      EST 18-AUG-2003
LOCUS         RCL1--04-J13.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION    Oryza sativa cDNA clone RCL1--04-J13, mRNA sequence.
ACCESSION     CF339347
VERSION       CF339347.1 GI:33827081
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
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REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE         Ehrhartoideae; Oryzeae; Oryza.
JOURNAL       1 (bases 1 to 17)
COMMENT       Kim,U.S., Yun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.
               Large-scale Sequencing Analysis of Rice ESTs
               Unpublished (2003)
               Contact: Nahm B.H.
               Genomics and Genetics Institute, Greengene Biotech Inc., Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES
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XhoI; cDNA was inserted into lambda Uni_ZAP XR vector at 5'
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Query Match      0.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4 CCTTTCCTCTCT 17
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RESULT 1749
AM249856      18 bp      mRNA      linear      EST 07-JAN-2000
LOCUS         2821566.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821566 3',
DEFINITION    mRNA sequence.
ACCESSION     AM249856
VERSION       AM249856.1 GI:6592849
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE         NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
               Other ESTs: 2821566.5prime
               Contact: Robert Strausberg, Ph.D.
               Email: cgaabs-remail.nih.gov
               Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
               Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
               Consortium (ULNL) DNA Sequencing by: Berkeley MGC sequencing
               project clone distribution: MGC clone distribution information can
               be found through the I.M.A.G.E. Consortium/ULNL at:
               www-bio.llnl.gov/bdrp/image/image.html Base Calling / Quality
               Scores: PHRED from University of Washington Genome Center. Vector
               Trimming: cross match from University of Washington Genome Center
               PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
               Drosophila Genome Project. University of Washington Genome Center:
               http://www.genome.washington.edu low Quality Sequence: 9 contiguous
               PHRED high quality bases following vector sequence. Very low
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Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCW7 row: C column: 7 High quality sequence stop: 9. Location/Qualifiers

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/clone\_lib="NH\_MGC-7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 14; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4470 TTTT TTTT TTTT TTTT TTTT G 4484  
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Db 1 TTTT TTTT TTTT TTTT G 15

RESULT 1750  
A2856873

LOCUS

A2856873 19 bp DNA linear GSS 21-FEB-2001

DEFINITION 2M0161019F Mouse 10kb plasmid UGCGM1 library Mus musculus genomic

clone UGCGM0161019 F, genomic survey sequence.

ACCESSION A2856873 GI:13048296

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0161 row: O column: 19

Seq primer: CGTGTGAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/clone\_lib="Mouse 10kb plasmid UGCGM1 library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT T 4477  
|||||  
Db 1 TTTT TTTT TTTT TTTT T 14

RESULT 1751  
A2950028

LOCUS

A2950028 19 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0213119R Mouse 10kb plasmid UGCGM1 library Mus musculus genomic

clone UGCGM0213119 R, genomic survey sequence.

ACCESSION A2950028 GI:13821255

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0213 row: L column: 19

Seq primer: CACACGGAACGACGTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGM0213119"

/sex="Female"  
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UGCG2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
|||||  
Db 19 TTTT TTTT TTTT 6

## RESULT 1752

CP301222 20 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-P21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--05-P21, mRNA sequence.

ACCESSION CP301222  
VERSION CP301222.1 GI:33672983  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretioideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Yun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of BioScience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

1..20

/organism="Oryza sativa"

/mol type="mRNA"

/culivar="Nackdong"

/db xref="taxon:4530"

/clone="7LEAF--05-P21"

/tissue\_type="leaf"

/dev stage="7 days after germination"

/lab host="E. coli DH10B"

/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOP0, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match

0.2%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477  
|||||  
Db 2 TTTT TTTT TTTT 15

## RESULT 1753

AZ832043 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M011211.F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG2M011211.F, genomic survey sequence.

ACCESSION AZ832043  
VERSION AZ832043.1 GI:13001951  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: 1 column: 11

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

location/Qualifiers

1..20

/organism="Mus musculus"

/mol type="genomic DNA"

/strain="C57BL/6J"

/db xref="taxon:10090"

/clone="UGCG2M011211"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3276 TTAGAGAGAAAT 3289  
 Db 17 TTAGAGAGAAAT 4

## RESULT 1754

AZ476017 21 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ476017  
 DEFINITION 1M0294C02R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0294C02 R, genomic survey sequence.

ACCESSION AZ476017  
 VERSION AZ476017.1 GI:10634142  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0294 row: C column: 02  
 Seq primer: CACACAGAAACGCTATAGCC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

## FEATURES

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0294C02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4471 TTTTTTTTTTTG 4484  
 Db 1 TTTTTTTTTTTG 14

## RESULT 1755

AZ589400 21 bp DNA linear GSS 13-DEC-2000  
 LOCUS AZ589400  
 DEFINITION 1M0398C23F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0398C23 F, genomic survey sequence.

ACCESSION AZ589400  
 VERSION AZ589400.1 GI:11711590  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0398 row: C column: 23  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

## FEATURES

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0398C23"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4463 CTTTTTTTTTTT 4476  
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 8 CTTTTTTTTTTT 21

DB 1 TTTTTTTTTTTT 14  
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RESULT 1756

Search completed: October 14, 2004, 13:12:42  
 Job time : 172 secs

LOCUS AZ785791 21 bp DNA linear GSS 16-FEB-2001  
 DEFINITION IM0030019F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0030019 F, genomic survey sequence.

ACCESSION AZ785791  
 VERSION AZ785791.1 GI:12922904  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niedermauser,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

TITLE University of Utah Genome Center  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0030 row: 0 column: 19  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
 source location/Qualifiers  
 1..21

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0030019"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
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 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4464 TTTTTTTTTTTT 4477



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 11:35:42 ; Search time 245 Seconds

(without alignments)  
3.666 Million cell updates/sec

Title: US-10-007-078-3

Perfect score: 7478  
Sequence: 1 actggcagctgcgcggcgccg.....acagtgccttattctta 7478

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 2960 seqs, 60060 residues

Total number of hits satisfying chosen parameters: 5920

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 3194 summaries

Database : rn13.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	26.2	0.4	33	1	US-09-475-947A-251
4	25.8	0.3	30	1	US-08-068-747-6
5	25.8	0.3	30	1	US-08-068-747-11
6	25.8	0.3	30	1	US-08-863-639A-30
7	25.8	0.3	30	1	US-09-135-99A-4
8	25.8	0.3	30	1	US-09-684-843A-4
9	25.8	0.3	31	1	US-08-570-155-14
10	25.8	0.3	31	1	PCT-US95-02861-14
11	25	0.3	33	1	US-08-068-747-7
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13	23.4	0.3	25	1	US-08-113-646A-42
14	23.4	0.3	33	1	US-08-465-384-4
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17	23.2	0.3	30	1	US-08-787-321-12
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24	22.8	0.3	35	1	US-08-173-489C-20
25	22.6	0.3	29	1	US-09-244-794A-8
26	22.6	0.3	29	1	US-09-007-005-8
27	22.6	0.3	29	1	US-09-247-190-8
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29	22.6	0.3	29	1	US-09-238-710-8
30	22.6	0.3	32	1	US-08-847-844A-94
31	22.2	0.3	29	1	US-09-750-401-10
32	22.2	0.3	32	1	US-10-003-998A-4
33	22	0.3	26	1	US-09-527-345-6
34					Sequence 10, Appli
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107	20.4	0.3	25	1	US-08-117-361C-3	Sequence 3, Appl1	C 180	19.8	0.3	28	1	US-08-863-028-21	Sequence 21, Appl1
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111	20.2	0.3	29	1	US-09-569-344-6	Sequence 6, Appl1	C 184	19.8	0.3	30	1	US-08-483-553-41	Sequence 41, Appl1
112	20	0.3	20	1	US-08-146-504-16	Sequence 16, Appl1	C 185	19.8	0.3	30	1	US-08-487-002-41	Sequence 41, Appl1
113	20	0.3	20	1	US-08-379-593-5	Sequence 5, Appl1	C 186	19.8	0.3	30	1	US-08-483-554B-41	Sequence 41, Appl1
114	20	0.3	20	1	US-08-725-976-16	Sequence 16, Appl1	C 187	19.8	0.3	30	1	US-08-488-011B-41	Sequence 41, Appl1
115	20	0.3	20	1	US-08-997-080-83	Sequence 83, Appl1	C 188	19.8	0.3	30	1	US-08-850-727-41	Sequence 41, Appl1
116	20	0.3	20	1	US-08-997-362-83	Sequence 83, Appl1	C 189	19.8	0.3	30	1	PCT-US95-10202-41	Sequence 41, Appl1
117	20	0.3	20	1	US-08-965-780-1	Sequence 1, Appl1	C 190	19.8	0.3	30	1	PCT-US95-10203-41	Sequence 41, Appl1
118	20	0.3	20	1	US-08-873-970-83	Sequence 83, Appl1	C 191	19.8	0.3	30	1	PCT-US95-10220-41	Sequence 41, Appl1
119	20	0.3	20	1	US-08-765-340-96	Sequence 96, Appl1	C 192	19.6	0.3	30	1	US-08-181-271A-85	Sequence 85, Appl1
120	20	0.3	20	1	US-09-095-855-83	Sequence 83, Appl1	C 193	19.6	0.3	30	1	US-08-449-315-85	Sequence 85, Appl1
121	20	0.3	20	1	US-09-407-675-1	Sequence 1, Appl1	C 194	19.6	0.3	30	1	US-08-449-043-85	Sequence 85, Appl1
122	20	0.3	20	1	US-09-250-075-1	Sequence 1, Appl1	C 195	19.6	0.3	30	1	US-08-449-043-85	Sequence 85, Appl1
123	20	0.3	20	1	US-09-173-936B-14	Sequence 14, Appl1	C 196	19.6	0.3	30	1	US-08-456-262A-85	Sequence 85, Appl1
124	20	0.3	20	1	US-09-454-704A-13	Sequence 13, Appl1	C 197	19.6	0.3	30	1	US-08-455-416-85	Sequence 85, Appl1
125	20	0.3	20	1	US-09-324-542-83	Sequence 83, Appl1	C 198	19.6	0.3	30	1	US-08-455-244-85	Sequence 85, Appl1
126	20	0.3	20	1	US-09-205-426-83	Sequence 83, Appl1	C 199	19.6	0.3	30	1	US-08-454-876-85	Sequence 85, Appl1
127	20	0.3	20	1	US-09-619-103-26	Sequence 26, Appl1	C 200	19.6	0.3	30	1	US-08-457-364-85	Sequence 85, Appl1
128	20	0.3	20	1	US-09-726-096A-1	Sequence 1, Appl1	C 201	19.6	0.3	30	1	US-08-456-262-85	Sequence 85, Appl1
129	20	0.3	20	1	US-09-603-830-55	Sequence 55, Appl1	C 202	19.6	0.3	30	1	US-08-456-240-85	Sequence 85, Appl1
130	20	0.3	20	1	US-09-976-978A-55	Sequence 55, Appl1	C 203	19.6	0.3	30	1	US-08-455-713-85	Sequence 85, Appl1
131	20	0.3	20	1	US-09-344-260A-10	Sequence 10, Appl1	C 204	19.6	0.3	30	1	US-08-971-217-85	Sequence 85, Appl1
132	20	0.3	20	1	US-09-961-949A-55	Sequence 55, Appl1	C 205	19.6	0.3	30	1	US-09-350-600-85	Sequence 85, Appl1
133	20	0.3	20	1	US-09-966-491A-55	Sequence 55, Appl1	C 206	19.6	0.3	30	1	US-09-350-600-85	Sequence 85, Appl1
134	20	0.3	20	1	US-09-957-313A-55	Sequence 55, Appl1	C 207	19.2	0.3	24	1	US-09-721-154-2	Sequence 2, Appl1
135	20	0.3	20	1	US-09-966-312-55	Sequence 55, Appl1	C 208	19.2	0.3	25	1	US-09-866-108A-13908	Sequence 13908, A
136	20	0.3	20	1	US-09-975-062A-55	Sequence 55, Appl1	C 209	19.2	0.3	25	1	US-09-866-108A-13909	Sequence 13909, A
137	20	0.3	20	1	US-09-976-971A-55	Sequence 55, Appl1	C 210	19.2	0.3	28	1	US-09-394-630-10	Sequence 10, Appl1
138	20	0.3	20	1	PCT-US93-07603-6	Sequence 6, Appl1	C 211	19.2	0.3	32	1	PCT-US92-10792-1	Sequence 1, Appl1
139	20	0.3	20	1	US-08-146-504-2	Sequence 2, Appl1	C 212	19.2	0.3	19	1	US-08-756-728A-1	Sequence 1, Appl1
140	20	0.3	20	1	US-08-455-896-13	Sequence 13, Appl1	C 213	19.2	0.3	19	1	US-08-469-852A-2	Sequence 2, Appl1
141	20	0.3	20	1	US-08-933-149-13	Sequence 13, Appl1	C 214	19.2	0.3	19	1	US-08-371-882B-16	Sequence 16, Appl1
142	20	0.3	20	1	US-08-725-976-2	Sequence 2, Appl1	C 215	19.2	0.3	19	1	US-08-295-509B-2	Sequence 2, Appl1
143	20	0.3	20	1	US-09-082-343-13	Sequence 13, Appl1	C 216	19.2	0.3	19	1	US-09-234-237-1	Sequence 1, Appl1
144	20	0.3	20	1	US-08-863-639A-13	Sequence 13, Appl1	C 217	19.2	0.3	19	1	US-09-016-520-20	Sequence 20, Appl1
145	20	0.3	20	1	US-08-863-639A-13	Sequence 13, Appl1	C 218	19.2	0.3	19	1	US-09-016-520-21	Sequence 21, Appl1
146	20	0.3	20	1	US-08-416-214A-12	Sequence 12, Appl1	C 219	19.2	0.3	19	1	US-09-016-520-22	Sequence 22, Appl1
147	20	0.3	20	1	US-09-082-253-13	Sequence 13, Appl1	C 220	19.2	0.3	19	1	US-09-016-520-23	Sequence 23, Appl1
148	20	0.3	20	1	US-08-271-862B-2	Sequence 2, Appl1	C 221	19.2	0.3	19	1	US-09-016-520-24	Sequence 24, Appl1
149	20	0.3	20	1	US-08-726-278-2	Sequence 2, Appl1	C 222	19.2	0.3	19	1	US-09-016-520-25	Sequence 25, Appl1
150	20	0.3	20	1	US-09-162-622-13	Sequence 13, Appl1	C 223	19.2	0.3	19	1	US-09-016-520-26	Sequence 26, Appl1
151	20	0.3	20	1	US-09-509-015-13	Sequence 13, Appl1	C 224	19.2	0.3	19	1	US-09-016-520-27	Sequence 27, Appl1
152	20	0.3	20	1	PCT-US96-08235-13	Sequence 13, Appl1	C 225	19.2	0.3	19	1	US-09-016-520-31	Sequence 31, Appl1
153	20	0.3	20	1	US-08-996-306-10	Sequence 10, Appl1	C 226	19.2	0.3	19	1	US-09-016-520-33	Sequence 33, Appl1
154	20	0.3	20	1	US-09-338-907-10	Sequence 10, Appl1	C 227	19.2	0.3	19	1	US-09-016-520-34	Sequence 34, Appl1
155	20	0.3	20	1	US-09-164-249B-6	Sequence 6, Appl1	C 228	19.2	0.3	19	1	US-09-016-520-44	Sequence 44, Appl1
156	20	0.3	20	1	US-09-218-207-10	Sequence 10, Appl1	C 229	19.2	0.3	19	1	US-09-378-568-4	Sequence 4, Appl1
157	20	0.3	20	1	US-08-771-781-2	Sequence 2, Appl1	C 230	19.2	0.3	19	1	US-09-130-973-20	Sequence 20, Appl1
158	20	0.3	20	1	US-09-011-143-23	Sequence 23, Appl1	C 231	19.2	0.3	19	1	US-09-130-973-21	Sequence 21, Appl1
159	20	0.3	20	1	US-09-725-265-4	Sequence 4, Appl1	C 232	19.2	0.3	19	1	US-09-130-973-22	Sequence 22, Appl1
160	20	0.3	20	1	US-09-725-265-5	Sequence 5, Appl1	C 233	19.2	0.3	19	1	US-09-130-973-23	Sequence 23, Appl1
161	20	0.3	20	1	US-09-725-265-6	Sequence 6, Appl1	C 234	19.2	0.3	19	1	US-09-130-973-24	Sequence 24, Appl1
162	20	0.3	20	1	US-09-725-265-7	Sequence 7, Appl1	C 235	19.2	0.3	19	1	US-09-130-973-25	Sequence 25, Appl1
163	20	0.3	20	1	US-09-725-265-8	Sequence 8, Appl1	C 236	19.2	0.3	19	1	US-09-130-973-26	Sequence 26, Appl1
164	20	0.3	20	1	US-09-725-265-9	Sequence 9, Appl1	C 237	19.2	0.3	19	1	US-09-130-973-27	Sequence 27, Appl1
165	20	0.3	20	1	US-09-725-265-10	Sequence 10, Appl1	C 238	19.2	0.3	19	1	US-09-130-973-31	Sequence 31, Appl1
166	20	0.3	20	1	US-09-725-265-11	Sequence 11, Appl1	C 239	19.2	0.3	19	1	US-09-130-973-33	Sequence 33, Appl1
167	20	0.3	20	1	US-09-725-265-12	Sequence 12, Appl1	C 240	19.2	0.3	19	1	US-09-130-973-34	Sequence 34, Appl1
168	20	0.3	20	1	US-09-725-265-13	Sequence 13, Appl1	C 241	19.2	0.3	19	1	US-09-130-973-40	Sequence 40, Appl1
169	20	0.3	20	1	US-09-303-465-23	Sequence 23, Appl1	C 242	19.2	0.3	19	1	US-09-477-902-20	Sequence 20, Appl1
170	20	0.3	20	1	US-10-079-616-23	Sequence 23, Appl1	C 243	19.2	0.3	19	1	US-09-477-902-21	Sequence 21, Appl1
171	19.8	0.3	24	1	US-08-906-156A-82	Sequence 82, Appl1	C 244	19.2	0.3	19	1	US-09-477-902-22	Sequence 22, Appl1
172	19.8	0.3	26	1	US-09-475-316A-59	Sequence 59, Appl1	C 245	19.2	0.3	19	1	US-09-477-902-23	Sequence 23, Appl1
173	19.8	0.3	26	1	US-09-704-640-59	Sequence 59, Appl1	C 246	19.2	0.3	19	1	US-09-477-902-24	Sequence 24, Appl1
174	19.8	0.3	27	1	US-08-821-451A-16	Sequence 16, Appl1	C 247	19.2	0.3	19	1	US-09-477-902-25	Sequence 25, Appl1
175	19.8	0.3	27	1	US-09-263-810-16	Sequence 16, Appl1	C 248	19.2	0.3	19	1	US-09-477-902-26	Sequence 26, Appl1
176	19.8	0.3	27	1	US-09-583-169-16	Sequence 16, Appl1	C 249	19.2	0.3	19	1	US-09-477-902-27	Sequence 27, Appl1
177	19.8	0.3	28	1	US-08-858-767-21	Sequence 21, Appl1	C 250	19.2	0.3	19	1	US-09-477-902-31	Sequence 31, Appl1
178	19.8	0.3	28	1	US-08-858-767-22	Sequence 22, Appl1	C 251	19.2	0.3	19	1	US-09-477-902-33	Sequence 33, Appl1
179	19.8	0.3	28	1	US-08-858-767-23	Sequence 23, Appl1	C 252	19.2	0.3	19	1	US-09-477-902-34	Sequence 34, Appl1

253	19	0.3	19	1	US-09-477-902-44	Sequence 44, Appl	326	18.8	0.3	26	1	US-08-978-121-1	Sequence 1, Appl
254	19	0.3	19	1	US-08-726-278-16	Sequence 16, Appl	327	18.6	0.2	27	1	US-08-584-040-6313	Sequence 6313, Ap
255	19	0.3	19	1	US-09-338-907-515	Sequence 515, App	328	18.6	0.2	28	1	US-08-858-767-14	Sequence 14, Appl
256	19	0.3	19	1	US-09-123-108-6	Sequence 6, Appl	329	18.6	0.2	28	1	US-08-863-028-14	Sequence 14, Appl
257	19	0.3	19	1	US-09-378-665A-5	Sequence 5, Appl	330	18.4	0.2	20	1	US-08-482-918-33	Sequence 33, Appl
258	19	0.3	19	1	US-09-203-294-4	Sequence 4, Appl	331	18.4	0.2	20	1	US-08-482-918-34	Sequence 34, Appl
259	19	0.3	19	1	US-09-218-207-515	Sequence 515, App	332	18.4	0.2	20	1	US-09-224-681-33	Sequence 33, Appl
260	19	0.3	19	1	US-09-303-586-15	Sequence 15, Appl	333	18.4	0.2	20	1	US-09-224-681-34	Sequence 34, Appl
261	19	0.3	19	1	US-09-303-586-16	Sequence 16, Appl	334	18.4	0.2	20	1	US-08-336-728A-33	Sequence 33, Appl
262	19	0.3	19	1	US-09-303-586-17	Sequence 17, Appl	335	18.4	0.2	20	1	US-08-336-728A-34	Sequence 34, Appl
263	19	0.3	19	1	US-09-303-586-18	Sequence 18, Appl	336	18.4	0.2	20	1	US-08-108-591B-4	Sequence 4, Appl
264	19	0.3	19	1	US-09-303-586-26	Sequence 26, Appl	337	18.4	0.2	20	1	US-09-588-950A-5	Sequence 5, Appl
265	19	0.3	19	1	US-09-227-782-1	Sequence 1, Appl	338	18.4	0.2	21	1	US-09-475-947A-119	Sequence 119, App
266	19	0.3	19	1	US-09-227-782-2	Sequence 2, Appl	339	18.4	0.2	22	1	US-08-123-449A-1	Sequence 1, Appl
267	19	0.3	19	1	US-09-227-782-3	Sequence 3, Appl	340	18.4	0.2	22	1	US-08-123-449A-2	Sequence 2, Appl
268	19	0.3	19	1	US-09-227-782-4	Sequence 4, Appl	341	18.4	0.2	22	1	US-08-458-050-1	Sequence 1, Appl
269	19	0.3	19	1	US-09-227-782-5	Sequence 5, Appl	342	18.4	0.2	22	1	US-08-458-050-2	Sequence 2, Appl
270	19	0.3	19	1	US-09-227-782-6	Sequence 6, Appl	343	18.4	0.2	22	1	US-08-950-196-1	Sequence 1, Appl
271	19	0.3	19	1	US-09-227-782-7	Sequence 7, Appl	344	18.4	0.2	22	1	US-08-950-196-2	Sequence 2, Appl
272	19	0.3	19	1	US-09-227-782-8	Sequence 8, Appl	345	18.2	0.2	19	1	US-08-881-784-18	Sequence 18, Appl
273	19	0.3	19	1	US-09-227-782-12	Sequence 12, Appl	346	18.2	0.2	19	1	US-09-232-768-18	Sequence 18, Appl
274	19	0.3	19	1	US-09-227-782-14	Sequence 14, Appl	347	18.2	0.2	23	1	US-08-242-664-1	Sequence 1, Appl
275	19	0.3	19	1	US-09-227-782-15	Sequence 15, Appl	348	18.2	0.2	23	1	US-08-484-138-1	Sequence 1, Appl
276	19	0.3	19	1	US-09-227-782-25	Sequence 25, Appl	349	18.2	0.2	23	1	PCT-US95-06379-1	Sequence 7, Appl
277	19	0.3	19	1	US-09-619-103-25	Sequence 25, Appl	350	18.2	0.2	24	1	US-09-721-154-7	Sequence 7, Appl
278	19	0.3	19	1	US-09-288-679-1	Sequence 1, Appl	351	18.2	0.2	25	1	US-08-374-144-3	Sequence 3, Appl
279	19	0.3	19	1	US-09-612-531-3	Sequence 3, Appl	352	18.2	0.2	25	1	US-08-775-164-3	Sequence 3, Appl
280	19	0.3	19	1	US-09-612-531-7	Sequence 7, Appl	353	18.2	0.2	25	1	US-08-775-609-3	Sequence 3, Appl
281	19	0.3	19	1	US-09-612-531-13	Sequence 13, Appl	354	18.2	0.2	25	1	US-08-775-607-3	Sequence 3, Appl
282	19	0.3	19	1	US-10-121-135-5	Sequence 5, Appl	355	18.2	0.2	25	1	US-09-866-108A-13907	Sequence 13907, A
283	19	0.3	19	1	US-10-121-135-5	Sequence 5, Appl	356	18.2	0.2	25	1	US-09-866-108A-13910	Sequence 13910, A
284	19	0.3	19	1	US-10-121-135-25	Sequence 25, Appl	357	18.2	0.2	25	1	PCT-US93-06828-3	Sequence 3, Appl
285	19	0.3	19	1	US-09-142-212A-10	Sequence 10, Appl	358	18	0.2	18	1	US-08-621-914A-16	Sequence 16, Appl
286	19	0.3	19	1	US-09-349-040A-3	Sequence 3, Appl	359	18	0.2	18	1	US-08-346-629-3	Sequence 3, Appl
287	19	0.3	19	1	US-09-349-040A-4	Sequence 4, Appl	360	18	0.2	18	1	US-08-358-556A-12	Sequence 12, Appl
288	19	0.3	19	1	US-09-349-040A-5	Sequence 5, Appl	361	18	0.2	18	1	US-08-358-556A-18	Sequence 18, Appl
289	19	0.3	19	1	US-09-409-926-17	Sequence 17, Appl	362	18	0.2	18	1	US-08-469-852A-4	Sequence 4, Appl
290	19	0.3	19	1	US-09-409-926-18	Sequence 18, Appl	363	18	0.2	18	1	US-08-863-639A-17	Sequence 17, Appl
291	19	0.3	19	1	US-10-123-597-1	Sequence 1, Appl	364	18	0.2	18	1	US-08-235-509B-4	Sequence 4, Appl
292	19	0.3	19	1	US-10-123-597-2	Sequence 2, Appl	365	18	0.2	18	1	US-08-884-029-9	Sequence 9, Appl
293	19	0.3	19	1	US-10-123-597-3	Sequence 3, Appl	366	18	0.2	18	1	US-08-941-445A-30	Sequence 30, Appl
294	19	0.3	19	1	US-10-123-597-4	Sequence 4, Appl	367	18	0.2	18	1	US-09-637-751A-3	Sequence 6, Appl
295	19	0.3	19	1	US-10-123-597-5	Sequence 5, Appl	368	18	0.2	18	1	US-09-545-225-9	Sequence 9, Appl
296	19	0.3	19	1	US-10-123-597-6	Sequence 6, Appl	369	18	0.2	18	1	US-09-619-103-24	Sequence 24, Appl
297	19	0.3	19	1	US-10-123-597-7	Sequence 7, Appl	370	18	0.2	18	1	US-09-370-541-14	Sequence 14, Appl
298	19	0.3	19	1	US-10-123-597-8	Sequence 8, Appl	371	18	0.2	18	1	US-10-125-295-9	Sequence 9, Appl
299	19	0.3	19	1	US-10-123-597-12	Sequence 12, Appl	372	18	0.2	18	1	PCT-US94-05407-4	Sequence 4, Appl
300	19	0.3	19	1	US-10-123-597-14	Sequence 14, Appl	373	18	0.2	19	1	US-09-435-806-7	Sequence 7, Appl
301	19	0.3	19	1	US-10-123-597-15	Sequence 15, Appl	374	18	0.2	26	1	US-08-487-41B-42	Sequence 42, Appl
302	19	0.3	19	1	US-10-123-597-25	Sequence 25, Appl	375	18	0.2	26	1	US-08-927-561-42	Sequence 42, Appl
303	19	0.3	19	1	US-09-349-033A-1	Sequence 1, Appl	376	18	0.2	26	1	PCT-US96-09388-42	Sequence 42, Appl
304	19	0.3	19	1	US-09-345-806-6	Sequence 6, Appl	377	18	0.2	27	1	US-08-946-914-50	Sequence 50, Appl
305	19	0.3	20	1	US-08-482-918-12	Sequence 32, Appl	378	18	0.2	27	1	US-08-584-040-1083	Sequence 1083, Ap
306	19	0.3	20	1	US-09-224-681-32	Sequence 32, Appl	379	18	0.2	27	1	US-08-584-040-7130	Sequence 7130, Ap
307	19	0.3	20	1	US-08-336-728A-32	Sequence 32, Appl	380	18	0.2	27	1	US-09-656-650-50	Sequence 50, Appl
308	19	0.3	21	1	US-08-359-295C-23	Sequence 23, Appl	381	17.8	0.2	21	1	US-09-422-878-9116	Sequence 9116, Ap
309	19	0.3	21	1	US-08-485-105A-23	Sequence 23, Appl	382	17.8	0.2	23	1	US-08-621-914A-6	Sequence 6, Appl
310	19	0.3	21	1	US-09-183-650-23	Sequence 23, Appl	383	17.8	0.2	23	1	US-09-056-052-9	Sequence 9, Appl
311	19	0.3	23	1	PCT-US94-05407-7	Sequence 7, Appl	384	17.8	0.2	24	1	US-08-938-803-60	Sequence 60, Appl
312	19	0.3	23	1	PCT-US94-05407-8	Sequence 8, Appl	385	17.8	0.2	24	1	US-09-688-990-2	Sequence 2, Appl
313	19	0.3	26	1	US-08-623-354-8	Sequence 8, Appl	386	17.8	0.2	25	1	US-08-811-492-41	Sequence 41, Appl
314	19	0.3	28	1	US-08-762-106-11	Sequence 11, Appl	387	17.8	0.2	25	1	US-09-866-108A-13911	Sequence 13911, A
315	19	0.3	28	1	US-09-320-774-11	Sequence 11, Appl	388	17.8	0.2	25	1	US-09-866-108A-13912	Sequence 13912, A
316	19	0.3	29	1	US-09-304-232-464	Sequence 464, Appl	389	17.8	0.2	25	1	PCT-US96-10545A-41	Sequence 41, Appl
317	18.8	0.3	23	1	US-08-018-129-15	Sequence 15, Appl	390	17.6	0.2	24	1	US-08-942-112B-5	Sequence 5, Appl
318	18.8	0.3	23	1	US-08-448-250-15	Sequence 15, Appl	391	17.6	0.2	25	1	US-09-596-120-18	Sequence 18, Appl
319	18.8	0.3	23	1	US-09-283-257-15	Sequence 15, Appl	392	17.6	0.2	25	1	US-09-596-120-19	Sequence 19, Appl
320	18.8	0.3	23	1	US-08-115-497-1	Sequence 1, Appl	393	17.6	0.2	26	1	US-07-885-570A-1	Sequence 1, Appl
321	18.8	0.3	25	1	US-08-466-670-1	Sequence 1, Appl	394	17.6	0.2	26	1	US-08-298-687A-1	Sequence 1, Appl
322	18.8	0.3	26	1	US-08-014-943A-21	Sequence 21, Appl	395	17.6	0.2	26	1	US-08-241-943-1	Sequence 1, Appl
323	18.8	0.3	26	1	US-08-486-421-15	Sequence 15, Appl	396	17.6	0.2	26	1	US-08-378-588-1	Sequence 1, Appl
324	18.8	0.3	26	1	US-08-470-911-15	Sequence 15, Appl	397	17.6	0.2	26	1	US-08-298-829-1	Sequence 1, Appl
325	18.8	0.3	26	1	US-08-486-809-15	Sequence 15, Appl	398	17.6	0.2	26	1	US-08-811-094-1	Sequence 1, Appl

399	17.6	0.2	26	1	US-08-467-504-10	Sequence 10, Appl	472	16.8	0.2	22	1	US-09-056-288A-30	Sequence 30, Appl
400	17.6	0.2	26	1	US-09-679-263-13	Sequence 13, Appl	473	16.8	0.2	23	1	US-08-068-945A-25	Sequence 25, Appl
401	17.6	0.2	26	1	PCT-US94-11121-1	Sequence 1, Appl	C 474	16.8	0.2	23	1	US-08-442-806-25	Sequence 25, Appl
402	17.6	0.2	27	1	US-08-985-162-999	Sequence 999, App	475	16.8	0.2	23	1	US-08-161-281A-10	Sequence 10, Appl
403	17.6	0.2	27	1	US-09-126-280-17	Sequence 17, Appl	476	16.8	0.2	25	1	US-08-648-709-4	Sequence 4, Appl
404	17.6	0.2	27	1	US-08-584-040-310	Sequence 310, App	C 477	16.8	0.2	25	1	US-09-010-641-34	Sequence 34, Appl
C 405	17.6	0.2	27	1	US-08-584-040-3684	Sequence 3684, Ap	C 478	16.8	0.2	25	1	US-09-356-281-34	Sequence 34, Appl
C 406	17.6	0.2	27	1	US-09-401-063-999	Sequence 999, App	479	16.8	0.2	25	1	US-09-393-389-4	Sequence 4, Appl
C 407	17.6	0.2	40	1	US-09-306-290-25	Sequence 25, App	480	16.8	0.2	25	1	US-08-866-108A-13913	Sequence 13913, A
408	17.4	0.2	19	1	US-08-410-540-5	Sequence 5, Appl	481	16.8	0.2	30	1	US-08-433-505-9	Sequence 9, Appl
409	17.4	0.2	20	1	US-07-912-900-20	Sequence 20, Appl	482	16.8	0.2	30	1	US-08-870-730-9	Sequence 9, Appl
410	17.4	0.2	20	1	US-08-285-309-20	Sequence 20, Appl	C 483	16.8	0.2	30	1	US-09-083-123-3	Sequence 3, Appl
411	17.4	0.2	20	1	US-08-313-075A-11	Sequence 11, Appl	C 484	16.8	0.2	30	1	US-09-083-123-7	Sequence 7, Appl
412	17.4	0.2	20	1	US-08-502-046-20	Sequence 20, Appl	485	16.8	0.2	30	1	US-08-882-649A-10	Sequence 10, Appl
413	17.4	0.2	20	1	US-08-927-219-56	Sequence 56, Appl	C 486	16.6	0.2	23	1	US-09-686-597-26	Sequence 26, Appl
414	17.4	0.2	23	1	US-08-621-914A-5	Sequence 5, Appl	C 487	16.6	0.2	23	1	US-09-083-268-11	Sequence 11, Appl
C 415	17.4	0.2	23	1	US-09-056-052-8	Sequence 8, Appl	C 488	16.6	0.2	24	1	US-08-529-190B-22	Sequence 22, Appl
C 416	17.4	0.2	27	1	US-09-475-947A-153	Sequence 153, App	489	16.6	0.2	24	1	US-08-863-639A-27	Sequence 27, Appl
C 417	17.4	0.2	35	1	US-08-173-489C-20	Sequence 20, Appl	490	16.6	0.2	24	1	US-09-157-210-4	Sequence 4, Appl
C 418	17.2	0.2	19	1	US-09-130-079-1	Sequence 1, Appl	491	16.6	0.2	24	1	US-09-581-493-9	Sequence 9, Appl
C 419	17.2	0.2	22	1	US-09-078-871A-3	Sequence 3, Appl	C 492	16.6	0.2	24	1	US-09-651-011A-5	Sequence 5, Appl
C 420	17.2	0.2	22	1	US-09-629-222A-7	Sequence 7, Appl	C 493	16.6	0.2	25	1	US-08-484-557C-12	Sequence 12, Appl
C 421	17.2	0.2	23	1	US-08-621-914A-4	Sequence 4, Appl	C 494	16.6	0.2	25	1	US-08-487-426B-12	Sequence 12, Appl
C 422	17.2	0.2	23	1	US-07-869-933-7	Sequence 7, Appl	C 495	16.6	0.2	25	1	US-08-487-720A-12	Sequence 12, Appl
C 423	17.2	0.2	23	1	US-09-056-052-7	Sequence 7, Appl	496	16.6	0.2	25	1	US-09-528-760A-10	Sequence 10, Appl
C 424	17.2	0.2	23	1	US-09-103-663-7	Sequence 7, Appl	497	16.6	0.2	25	1	US-09-951-843-10	Sequence 10, Appl
C 425	17.2	0.2	23	1	US-09-632-098-24	Sequence 24, Appl	C 498	16.6	0.2	25	1	US-09-866-108A-3233	Sequence 3233, Ap
426	17.2	0.2	24	1	US-08-356-790-9	Sequence 9, Appl	C 499	16.6	0.2	25	1	US-09-866-108A-3234	Sequence 3234, Ap
C 427	17.2	0.2	24	1	US-09-360-545-100	Sequence 100, App	C 500	16.6	0.2	25	1	US-09-866-108A-3335	Sequence 3235, Ap
428	17.2	0.2	24	1	US-09-360-545-101	Sequence 101, App	C 501	16.6	0.2	25	1	US-09-866-108A-4407	Sequence 4407, Ap
429	17.2	0.2	24	1	US-09-496-632C-11	Sequence 11, Appl	C 502	16.6	0.2	25	1	US-09-866-108A-4408	Sequence 4408, Ap
430	17.2	0.2	24	1	US-09-496-632C-12	Sequence 12, Appl	C 503	16.6	0.2	25	1	US-09-866-108A-4409	Sequence 4409, Ap
431	17.2	0.2	25	1	US-09-380-6420C-11	Sequence 11, Appl	504	16.6	0.2	25	1	US-09-866-108A-5201	Sequence 5201, Ap
432	17.2	0.2	25	1	US-09-899-642A-11	Sequence 11, Appl	505	16.6	0.2	25	1	US-09-866-108A-5202	Sequence 5202, Ap
433	17.2	0.2	25	1	US-09-866-108A-13906	Sequence 13906, A	506	16.6	0.2	25	1	US-09-866-108A-5203	Sequence 5203, Ap
434	17.2	0.2	26	1	US-08-632-575B-7	Sequence 7, Appl	507	16.6	0.2	25	1	US-09-866-108A-12694	Sequence 12694, A
435	17.2	0.2	26	1	US-08-747-536-17	Sequence 17, Appl	508	16.6	0.2	25	1	US-09-866-108A-12695	Sequence 12695, A
436	17.2	0.2	26	1	US-09-199-542B-7	Sequence 7, Appl	509	16.6	0.2	32	1	US-10-003-998A-4	Sequence 4, Appl
C 437	17.2	0.2	30	1	US-09-725-265-11	Sequence 11, Appl	C 510	16.4	0.2	18	1	US-08-679-645-1167	Sequence 1167, Ap
C 438	17.2	0.2	30	1	US-09-725-265-13	Sequence 13, Appl	511	16.4	0.2	18	1	US-09-205-995-48	Sequence 48, Appl
C 439	17.2	0.2	33	1	US-09-061-026-26	Sequence 26, Appl	512	16.4	0.2	19	1	US-09-422-978-110119	Sequence 10119, A
C 440	17.2	0.2	33	1	US-09-466-138-26	Sequence 26, Appl	513	16.4	0.2	20	1	US-08-275-951-49	Sequence 49, Appl
441	17	0.2	17	1	US-08-851-843A-132	Sequence 132, App	C 514	16.4	0.2	21	1	US-08-628-540-3	Sequence 8, Appl
442	17	0.2	17	1	US-09-250-075-5	Sequence 5, Appl	C 515	16.4	0.2	21	1	US-08-941-100-8	Sequence 3, Appl
443	17	0.2	17	1	US-08-854-050-132	Sequence 132, App	516	16.4	0.2	23	1	US-09-161-466-19	Sequence 19, Appl
444	17	0.2	17	1	US-09-430-323-132	Sequence 132, App	C 517	16.4	0.2	24	1	US-09-360-416-74	Sequence 74, Appl
445	17	0.2	17	1	US-08-584-040-2549	Sequence 2549, Ap	C 518	16.4	0.2	25	1	US-08-367-101-140	Sequence 140, App
446	17	0.2	17	1	US-08-584-040-2550	Sequence 2550, Ap	C 519	16.4	0.2	25	1	US-08-592-541-140	Sequence 140, App
C 447	17	0.2	17	1	US-09-619-103-23	Sequence 23, Appl	C 520	16.4	0.2	25	1	US-09-124-698-140	Sequence 140, App
448	17	0.2	17	1	US-09-726-096A-5	Sequence 5, Appl	C 521	16.4	0.2	25	1	US-09-127-480-140	Sequence 140, App
449	17	0.2	17	1	US-09-371-772B-1073	Sequence 1073, Ap	C 522	16.4	0.2	25	1	US-08-496-843C-140	Sequence 140, App
450	17	0.2	17	1	US-09-371-772B-1074	Sequence 1074, Ap	C 523	16.4	0.2	25	1	US-09-124-523-140	Sequence 140, App
451	17	0.2	18	1	US-09-637-751A-5	Sequence 5, Appl	C 524	16.4	0.2	25	1	US-09-636-796A-140	Sequence 140, App
452	17	0.2	19	1	US-08-973-857-6	Sequence 6, Appl	C 525	16.2	0.2	21	1	US-08-294-424-27	Sequence 27, Appl
C 453	17	0.2	20	1	US-09-198-452A-3717	Sequence 3717, Ap	526	16.2	0.2	21	1	US-08-472-651-20	Sequence 20, Appl
454	17	0.2	21	1	US-08-704-966-7	Sequence 7, Appl	527	16.2	0.2	21	1	US-08-474-661-20	Sequence 20, Appl
455	17	0.2	21	1	US-08-705-438-7	Sequence 7, Appl	528	16.2	0.2	21	1	US-08-611-977-20	Sequence 20, Appl
456	17	0.2	25	1	US-09-866-108A-5298	Sequence 5298, Ap	C 529	16.2	0.2	21	1	US-08-863-639A-52	Sequence 52, Appl
457	17	0.2	25	1	US-09-866-108A-5299	Sequence 5299, Ap	C 530	16.2	0.2	21	1	US-08-863-639A-55	Sequence 55, Appl
458	17	0.2	25	1	US-09-866-108A-12696	Sequence 12696, A	C 531	16.2	0.2	21	1	US-08-863-639A-67	Sequence 67, Appl
459	17	0.2	25	1	US-09-866-108A-12697	Sequence 12697, A	C 532	16.2	0.2	21	1	US-08-863-639A-68	Sequence 68, Appl
C 460	17	0.2	25	1	US-09-866-108A-13467	Sequence 13467, A	533	16.2	0.2	21	1	US-08-863-639A-71	Sequence 71, Appl
461	17	0.2	26	1	US-08-291-011-10	Sequence 10, Appl	534	16.2	0.2	21	1	US-08-616-214A-11	Sequence 11, Appl
462	17	0.2	26	1	US-09-282-147-1	Sequence 1, Appl	535	16.2	0.2	21	1	US-08-428-942-8	Sequence 8, Appl
463	17	0.2	26	1	US-09-266-065-10	Sequence 10, Appl	536	16.2	0.2	21	1	US-09-922-978-11535	Sequence 11535, A
C 464	17	0.2	26	1	US-09-538-709-415	Sequence 415, Appl	537	16.2	0.2	21	1	US-09-422-978-11535	Sequence 7, Appl
465	17	0.2	30	1	US-09-935-265-10	Sequence 10, Appl	C 538	16.2	0.2	22	1	US-08-390-850-7	Sequence 7, Appl
C 466	17	0.2	30	1	US-09-725-265-10	Sequence 10, Appl	C 539	16.2	0.2	22	1	US-08-435-634-7	Sequence 7, Appl
C 467	17	0.2	30	1	US-09-725-265-12	Sequence 12, Appl	C 540	16.2	0.2	22	1	US-09-009-913-156	Sequence 156, App
C 468	17	0.2	31	1	US-09-268-505B-13	Sequence 13, Appl	541	16.2	0.2	23	1	US-09-230-222-16	Sequence 23, Appl
C 469	16.8	0.2	20	1	US-08-568-271-1	Sequence 1, Appl	542	16.2	0.2	23	1	US-09-230-225B-23	Sequence 23, Appl
470	16.8	0.2	20	1	US-09-661-753-35	Sequence 35, Appl	C 543	16.2	0.2	23	1	US-09-686-597-24	Sequence 24, Appl
471	16.8	0.2	20	1	US-09-723-368-5	Sequence 5, Appl	C 544	16.2	0.2	23	1	US-09-686-597-25	Sequence 25, Appl

C 545	16.2	0.2	23	1	US-09-686-597-27	Sequence 27, Appl	C 618	15.8	0.2	20	1	US-09-357-070-22	Sequence 22, Appl
C 546	16.2	0.2	24	1	US-08-465-590-94	Sequence 94, Appl	C 619	15.8	0.2	20	1	US-09-287-796-14	Sequence 14, Appl
C 547	16.2	0.2	24	1	US-08-570-155-16	Sequence 16, Appl	C 620	15.8	0.2	20	1	US-09-444-053-26	Sequence 26, Appl
C 548	16.2	0.2	24	1	US-08-487-799-17	Sequence 17, Appl	C 621	15.8	0.2	20	1	US-09-030-701-65	Sequence 65, Appl
C 549	16.2	0.2	24	1	US-09-030-701-29	Sequence 29, Appl	C 622	15.8	0.2	20	1	US-09-130-616-14	Sequence 14, Appl
C 550	16.2	0.2	24	1	US-09-286-098-61	Sequence 61, Appl	C 623	15.8	0.2	20	1	US-09-657-042A-39	Sequence 39, Appl
C 551	16.2	0.2	24	1	US-08-711-417C-94	Sequence 94, Appl	C 624	15.8	0.2	20	1	US-09-082-649B-57	Sequence 57, Appl
C 552	16.2	0.2	24	1	US-08-960-774-61	Sequence 61, Appl	C 625	15.8	0.2	20	1	US-09-232-146-59	Sequence 59, Appl
C 553	16.2	0.2	24	1	US-09-296-280-48	Sequence 48, Appl	C 626	15.8	0.2	20	1	US-09-732-199A-54	Sequence 54, Appl
C 554	16.2	0.2	24	1	US-09-325-193A-52	Sequence 52, Appl	C 627	15.8	0.2	20	1	US-08-108-591B-5	Sequence 5, Appl
C 555	16.2	0.2	24	1	US-09-191-170-55	Sequence 55, Appl	C 628	15.8	0.2	20	1	US-09-535-008-11	Sequence 11, Appl
C 556	16.2	0.2	24	1	US-09-723-909-94	Sequence 94, Appl	C 629	15.8	0.2	20	1	US-09-690-364-59	Sequence 99, Appl
C 557	16.2	0.2	24	1	US-09-337-619-61	Sequence 61, Appl	C 630	15.8	0.2	20	1	US-09-725-265-35	Sequence 35, Appl
C 558	16.2	0.2	25	1	PCT-US93-08743-94	Sequence 94, Appl	C 631	15.8	0.2	21	1	US-09-422-978-7625	Sequence 7625, Ap
C 559	16.2	0.2	25	1	US-08-115-497-1	Sequence 1, Appl	C 632	15.8	0.2	21	1	US-09-422-978-9563	Sequence 9563, Ap
C 560	16.2	0.2	25	1	US-08-466-670-1	Sequence 1, Appl	C 633	15.8	0.2	21	1	US-09-422-978-10315	Sequence 10315, A
C 561	16.2	0.2	16	1	US-08-087-387-6	Sequence 6, Appl	C 634	15.8	0.2	22	1	US-08-546-130A-23	Sequence 23, Appl
C 562	16.2	0.2	16	1	US-08-455-627-6	Sequence 6, Appl	C 635	15.8	0.2	22	1	US-08-680-395-11	Sequence 31, Appl
C 563	16.2	0.2	16	1	US-07-971-978-36	Sequence 36, Appl	C 636	15.8	0.2	22	1	US-08-291-011-9	Sequence 9, Appl
C 564	16.2	0.2	16	1	US-07-971-978-42	Sequence 42, Appl	C 637	15.8	0.2	22	1	US-09-066-641-12	Sequence 12, Appl
C 565	16.2	0.2	16	1	US-07-971-978-60	Sequence 60, Appl	C 638	15.8	0.2	22	1	US-09-266-065-9	Sequence 9, Appl
C 566	16.2	0.2	16	1	US-08-461-271-6	Sequence 6, Appl	C 639	15.8	0.2	22	1	US-09-935-247-9	Sequence 9, Appl
C 567	16.2	0.2	16	1	US-08-415-370-2	Sequence 2, Appl	C 640	15.8	0.2	23	1	US-09-262-773-203	Sequence 203, App
C 568	16.2	0.2	16	1	US-08-713-685A-6	Sequence 6, Appl	C 641	15.8	0.2	23	1	US-08-934-386-30	Sequence 30, Appl
C 569	16.2	0.2	16	1	US-08-689-856-6	Sequence 6, Appl	C 642	15.8	0.2	23	1	US-10-238-483-1	Sequence 1, Appl
C 570	16.2	0.2	16	1	US-08-687-551-15	Sequence 15, Appl	C 643	15.8	0.2	24	1	US-08-520-928-3	Sequence 3, Appl
C 571	16.2	0.2	16	1	US-09-070-477-6	Sequence 6, Appl	C 644	15.8	0.2	24	1	US-08-570-155-17	Sequence 17, Appl
C 572	16.2	0.2	16	1	US-09-141-764-2	Sequence 2, Appl	C 645	15.8	0.2	24	1	US-09-004-113-23	Sequence 23, Appl
C 573	16.2	0.2	16	1	US-08-851-843A-131	Sequence 131, App	C 646	15.8	0.2	24	1	US-08-974-549A-472	Sequence 472, App
C 574	16.2	0.2	16	1	US-08-854-050-131	Sequence 131, App	C 647	15.8	0.2	24	1	US-08-912-951-339	Sequence 339, App
C 575	16.2	0.2	16	1	US-09-430-323-131	Sequence 131, App	C 648	15.8	0.2	24	1	US-09-402-181B-472	Sequence 472, App
C 576	16.2	0.2	16	1	US-09-507-345A-2	Sequence 2, Appl	C 649	15.8	0.2	24	1	US-09-721-456-472	Sequence 472, App
C 577	16.2	0.2	16	1	US-09-619-103-22	Sequence 22, Appl	C 650	15.8	0.2	27	1	US-08-208-486-79	Sequence 79, Appl
C 578	16.2	0.2	16	1	US-09-739-928-2	Sequence 2, Appl	C 651	15.8	0.2	29	1	US-09-244-794A-8	Sequence 8, Appl
C 579	16.2	0.2	17	1	US-08-821-827C-30	Sequence 30, Appl	C 652	15.8	0.2	29	1	US-09-007-005-8	Sequence 8, Appl
C 580	16.2	0.2	17	1	US-09-290-202B-30	Sequence 30, Appl	C 653	15.8	0.2	29	1	US-09-247-190-8	Sequence 8, Appl
C 581	16.2	0.2	17	1	US-08-584-040-2548	Sequence 2548, Ap	C 654	15.8	0.2	29	1	US-09-244-796-8	Sequence 8, Appl
C 582	16.2	0.2	17	1	US-08-584-040-2551	Sequence 2551, Ap	C 655	15.8	0.2	29	1	US-09-238-710-8	Sequence 8, Appl
C 583	16.2	0.2	17	1	US-09-788-338-3	Sequence 3, Appl	C 656	15.8	0.2	29	1	US-09-282-734-3	Sequence 3, Appl
C 584	16.2	0.2	17	1	US-09-300-958A-64	Sequence 64, Appl	C 657	15.8	0.2	29	1	US-08-400-275-13	Sequence 13, Appl
C 585	16.2	0.2	17	1	US-09-371-772B-1072	Sequence 1072, Ap	C 658	15.8	0.2	29	1	US-08-910-632-6	Sequence 6, Appl
C 586	16.2	0.2	17	1	US-09-371-772B-1075	Sequence 1075, Ap	C 659	15.8	0.2	29	1	US-08-805-631A-6	Sequence 6, Appl
C 587	16.2	0.2	18	1	US-08-927-274A-6	Sequence 6, Appl	C 660	15.8	0.2	29	1	US-09-569-344-6	Sequence 6, Appl
C 588	16.2	0.2	18	1	US-09-637-751A-7	Sequence 7, Appl	C 661	15.8	0.2	30	1	US-09-648-040-4	Sequence 4, Appl
C 589	16.2	0.2	18	1	US-09-422-978-4670	Sequence 4670, Ap	C 662	15.8	0.2	30	1	US-09-725-265-9	Sequence 9, Appl
C 590	16.2	0.2	20	1	US-08-650-598-8	Sequence 8, Appl	C 663	15.8	0.2	32	1	US-09-750-401-10	Sequence 10, Appl
C 591	16.2	0.2	20	1	US-09-228-942-7	Sequence 7, Appl	C 664	15.8	0.2	33	1	5478746-1	Patent No. 5478746
C 592	16.2	0.2	20	1	US-09-965-599-4	Sequence 4, Appl	C 665	15.6	0.2	22	1	US-08-937-067-17	Sequence 17, Appl
C 593	16.2	0.2	20	1	US-09-198-452A-4311	Sequence 4311, Ap	C 666	15.6	0.2	22	1	US-08-056-200-35	Sequence 35, Appl
C 594	16.2	0.2	22	1	US-08-318-837-37	Sequence 37, Appl	C 667	15.6	0.2	22	1	US-08-056-200-39	Sequence 39, Appl
C 595	16.2	0.2	24	1	US-08-863-639A-27	Sequence 27, Appl	C 668	15.6	0.2	22	1	US-08-410-540-20	Sequence 20, Appl
C 596	16.2	0.2	24	1	US-08-200-807-3	Sequence 3, Appl	C 669	15.6	0.2	22	1	US-08-459-999-1	Sequence 1, Appl
C 597	16.2	0.2	24	1	US-08-242-402-13	Sequence 13, Appl	C 670	15.6	0.2	22	1	US-08-800-644-35	Sequence 35, Appl
C 598	16.2	0.2	24	1	US-08-488-305A-3	Sequence 3, Appl	C 671	15.6	0.2	22	1	US-08-800-644-39	Sequence 39, Appl
C 599	16.2	0.2	24	1	US-08-808-474A-9	Sequence 9, Appl	C 672	15.6	0.2	22	1	US-08-964-143-1	Sequence 1, Appl
C 600	16.2	0.2	24	1	US-08-808-474A-10	Sequence 10, Appl	C 673	15.6	0.2	22	1	US-09-344-667-43	Sequence 43, Appl
C 601	16.2	0.2	24	1	US-08-682-423-26	Sequence 26, Appl	C 674	15.6	0.2	22	1	US-09-344-667-46	Sequence 46, Appl
C 602	16.2	0.2	24	1	US-09-142-521-6	Sequence 6, Appl	C 675	15.6	0.2	22	1	US-09-693-352-43	Sequence 43, Appl
C 603	16.2	0.2	24	1	US-09-235-614-10	Sequence 10, Appl	C 676	15.6	0.2	22	1	US-09-693-352-46	Sequence 46, Appl
C 604	16.2	0.2	24	1	US-09-235-614-11	Sequence 11, Appl	C 677	15.6	0.2	22	1	US-09-693-005A-43	Sequence 43, Appl
C 605	16.2	0.2	24	1	US-09-018-584A-92	Sequence 92, Appl	C 678	15.6	0.2	22	1	US-09-693-005A-46	Sequence 46, Appl
C 606	16.2	0.2	24	1	US-09-298-886-6	Sequence 6, Appl	C 679	15.6	0.2	22	1	US-09-603-830-43	Sequence 43, Appl
C 607	16.2	0.2	24	1	US-09-006-755B-10	Sequence 10, Appl	C 680	15.6	0.2	22	1	US-09-603-830-46	Sequence 46, Appl
C 608	16.2	0.2	24	1	US-09-356-806-82	Sequence 82, Appl	C 681	15.6	0.2	22	1	US-09-603-830-46	Sequence 46, Appl
C 609	16.2	0.2	24	1	US-09-999-672-6	Sequence 6, Appl	C 682	15.6	0.2	22	1	US-09-976-978A-43	Sequence 43, Appl
C 610	16.2	0.2	24	1	PCT-US93-08329-4	Sequence 4, Appl	C 683	15.6	0.2	22	1	US-09-976-978A-46	Sequence 46, Appl
C 611	16.2	0.2	24	1	PCT-US95-05141-26	Sequence 26, Appl	C 684	15.6	0.2	22	1	US-09-961-949A-43	Sequence 43, Appl
C 612	15.8	0.2	19	1	US-09-422-978-5276	Sequence 5276, Ap	C 685	15.6	0.2	22	1	US-09-961-949A-46	Sequence 46, Appl
C 613	15.8	0.2	20	1	US-08-117-952-613	Sequence 613, App	C 686	15.6	0.2	22	1	US-09-966-491A-43	Sequence 43, Appl
C 614	15.8	0.2	20	1	US-08-173-489C-18	Sequence 18, Appl	C 687	15.6	0.2	22	1	US-09-966-491A-46	Sequence 46, Appl
C 615	15.8	0.2	20	1	US-08-910-629A-14	Sequence 14, Appl	C 688	15.6	0.2	22	1	US-09-611-627-49	Sequence 49, Appl
C 616	15.8	0.2	20	1	US-08-507-032-8	Sequence 8, Appl	C 689	15.6	0.2	22	1	US-09-957-113A-43	Sequence 43, Appl
C 617	15.8	0.2	20	1	US-08-914-961-2	Sequence 2, Appl	C 690	15.6	0.2	22	1	US-09-957-113A-46	Sequence 46, Appl

C 691	15.6	0.2	22	1	US-09-966-312-43	Sequence 43, Appl	C 764	15.4	0.2	19	1	US-09-814-988-39	Sequence 39, Appl
C 692	15.6	0.2	22	1	US-09-966-312-46	Sequence 46, Appl	C 765	15.4	0.2	19	1	US-09-530-098B-26	Sequence 26, Appl
C 693	15.6	0.2	22	1	US-09-975-062A-43	Sequence 43, Appl	C 766	15.4	0.2	20	1	US-08-715-461-5	Sequence 5, Appl
C 694	15.6	0.2	22	1	US-09-975-062A-46	Sequence 46, Appl	C 767	15.4	0.2	20	1	US-09-517-584A-13	Sequence 13, Appl
C 695	15.6	0.2	22	1	US-09-976-971A-43	Sequence 43, Appl	C 768	15.4	0.2	20	1	US-09-021-701-728	Sequence 728, App
C 696	15.6	0.2	22	1	US-09-976-971A-46	Sequence 46, Appl	C 769	15.4	0.2	20	1	US-09-021-701-739	Sequence 729, App
C 697	15.6	0.2	23	1	US-08-025-038-2	Sequence 2, Appl	C 770	15.4	0.2	20	1	US-09-021-701-730	Sequence 730, App
C 698	15.6	0.2	23	1	US-08-484-557C-13	Sequence 13, Appl	C 771	15.4	0.2	20	1	US-09-021-701-731	Sequence 731, App
C 699	15.6	0.2	23	1	US-08-487-426B-13	Sequence 13, Appl	C 772	15.4	0.2	20	1	US-09-844-63A-46	Sequence 46, Appl
C 700	15.6	0.2	23	1	US-08-659-605A-19	Sequence 19, Appl	C 773	15.4	0.2	20	1	US-09-792-59A-20	Sequence 20, Appl
C 701	15.6	0.2	23	1	US-08-450-945-52	Sequence 52, Appl	C 774	15.4	0.2	20	1	US-09-907-843-23	Sequence 23, Appl
C 702	15.6	0.2	23	1	US-08-487-720A-13	Sequence 13, Appl	C 775	15.4	0.2	20	1	US-09-470-443-17	Sequence 17, Appl
C 703	15.6	0.2	23	1	US-08-637-115-3	Sequence 3, Appl	C 776	15.4	0.2	20	1	US-09-300-008B-19	Sequence 39, Appl
C 704	15.6	0.2	23	1	US-08-976-161-52	Sequence 52, Appl	C 777	15.4	0.2	20	1	US-09-844-525A-79	Sequence 79, Appl
C 705	15.6	0.2	23	1	US-09-338-907-461	Sequence 461, App	C 778	15.4	0.2	20	1	US-09-422-978-6348	Sequence 6348, Ap
C 706	15.6	0.2	23	1	US-09-282-147-30	Sequence 30, Appl	C 779	15.4	0.2	20	1	US-09-601-144-22	Sequence 22, Appl
C 707	15.6	0.2	23	1	US-09-218-207-461	Sequence 461, App	C 780	15.4	0.2	20	1	US-09-903-413-8	Sequence 8, Appl
C 708	15.6	0.2	23	1	US-09-395-604A-3	Sequence 3, Appl	C 781	15.4	0.2	21	1	US-08-665-615B-177	Sequence 177, App
C 709	15.6	0.2	23	1	US-08-650-965-4	Sequence 4, Appl	C 782	15.4	0.2	21	1	US-08-467-346-43	Sequence 43, Appl
C 710	15.6	0.2	23	1	US-09-687-910-3	Sequence 3, Appl	C 783	15.4	0.2	21	1	US-08-628-540-9	Sequence 9, Appl
C 711	15.6	0.2	24	1	US-08-014-943A-11	Sequence 11, Appl	C 784	15.4	0.2	21	1	US-08-941-100-4	Sequence 4, Appl
C 712	15.6	0.2	24	1	US-08-486-421-46	Sequence 46, Appl	C 785	15.4	0.2	21	1	US-08-941-100-4	Sequence 9992, Ap
C 713	15.6	0.2	24	1	US-08-411-796-187	Sequence 187, App	C 786	15.4	0.2	21	1	US-09-422-978-9992	Sequence 11139, A
C 714	15.6	0.2	24	1	US-08-470-911-46	Sequence 46, Appl	C 787	15.4	0.2	21	1	US-09-536-393-23	Sequence 23, Appl
C 715	15.6	0.2	24	1	US-08-662-335A-1	Sequence 1, Appl	C 788	15.4	0.2	21	1	US-09-536-393-29	Sequence 29, Appl
C 716	15.6	0.2	24	1	US-08-808-474A-8	Sequence 8, Appl	C 789	15.4	0.2	22	1	US-08-657-272B-18	Sequence 18, Appl
C 717	15.6	0.2	24	1	US-08-808-474A-11	Sequence 11, Appl	C 790	15.4	0.2	22	1	US-08-761-704-5	Sequence 5, Appl
C 718	15.6	0.2	24	1	US-08-486-809-46	Sequence 46, Appl	C 791	15.4	0.2	22	1	US-08-722-240-2	Sequence 2, Appl
C 719	15.6	0.2	24	1	US-08-859-998-893	Sequence 893, App	C 792	15.4	0.2	22	1	US-09-095-372-5	Sequence 5, Appl
C 720	15.6	0.2	24	1	US-08-924-695A-22	Sequence 22, Appl	C 793	15.4	0.2	22	1	US-08-182-172-16	Sequence 16, Appl
C 721	15.6	0.2	24	1	US-08-471-039-187	Sequence 187, App	C 794	15.4	0.2	23	1	US-09-870-956-41	Sequence 41, Appl
C 722	15.6	0.2	24	1	US-08-624-290B-9	Sequence 9, Appl	C 795	15.4	0.2	23	1	US-09-325-554-18	Sequence 18, Appl
C 723	15.6	0.2	24	1	US-09-235-614-8	Sequence 8, Appl	C 796	15.4	0.2	27	1	US-09-725-265-8	Sequence 8, Appl
C 724	15.6	0.2	24	1	US-09-235-614-9	Sequence 9, Appl	C 797	15.4	0.2	30	1	US-09-619-103-14	Sequence 14, Appl
C 725	15.6	0.2	24	1	US-09-463-702A-8	Sequence 8, Appl	C 798	15.4	0.2	32	1	US-09-930-324B-2	Sequence 2, Appl
C 726	15.6	0.2	24	1	US-09-225-928-893	Sequence 893, App	C 799	15.2	0.2	17	1	US-10-015-593-2	Sequence 2, Appl
C 727	15.6	0.2	24	1	US-09-487-130-1	Sequence 1, Appl	C 800	15.2	0.2	20	1	US-08-031-143B-12	Sequence 12, Appl
C 728	15.6	0.2	24	1	US-09-487-130-2	Sequence 2, Appl	C 801	15.2	0.2	20	1	US-08-564-002-11	Sequence 12, Appl
C 729	15.6	0.2	24	1	US-09-487-130-3	Sequence 3, Appl	C 802	15.2	0.2	20	1	US-08-890-980-61	Sequence 61, Appl
C 730	15.6	0.2	24	1	US-09-487-130-4	Sequence 4, Appl	C 803	15.2	0.2	20	1	US-09-226-568-37	Sequence 37, Appl
C 731	15.6	0.2	24	1	US-09-487-130-5	Sequence 5, Appl	C 804	15.2	0.2	20	1	US-08-890-979-61	Sequence 61, Appl
C 732	15.6	0.2	24	1	US-09-487-130-6	Sequence 6, Appl	C 805	15.2	0.2	20	1	US-09-289-267-56	Sequence 56, Appl
C 733	15.6	0.2	24	1	US-09-641-318-22	Sequence 22, Appl	C 806	15.2	0.2	20	1	US-09-032-894-61	Sequence 61, Appl
C 734	15.6	0.2	24	1	US-08-985-492-24	Sequence 24, Appl	C 807	15.2	0.2	20	1	US-08-765-340-10	Sequence 10, Appl
C 735	15.6	0.2	24	1	US-09-699-135-8	Sequence 8, Appl	C 808	15.2	0.2	20	1	US-09-407-675-2	Sequence 7, Appl
C 736	15.6	0.2	24	1	US-08-559-390-187	Sequence 187, App	C 809	15.2	0.2	20	1	US-09-429-322-70	Sequence 70, Appl
C 737	15.6	0.2	24	1	US-09-225-201B-893	Sequence 893, App	C 810	15.2	0.2	20	1	US-09-031-626-61	Sequence 61, Appl
C 738	15.6	0.2	24	1	PCT-US93-11198-187	Sequence 187, App	C 811	15.2	0.2	20	1	US-09-110-517-42	Sequence 42, Appl
C 739	15.6	0.2	30	1	US-09-725-265-5	Sequence 5, Appl	C 812	15.2	0.2	20	1	US-09-021-701-732	Sequence 732, App
C 740	15.6	0.2	30	1	US-09-725-265-6	Sequence 6, Appl	C 813	15.2	0.2	20	1	US-09-021-701-733	Sequence 733, App
C 741	15.6	0.2	30	1	US-09-725-265-7	Sequence 7, Appl	C 814	15.2	0.2	20	1	US-09-021-701-734	Sequence 734, App
C 742	15.6	0.2	17	1	US-08-242-664-23	Sequence 23, Appl	C 815	15.2	0.2	20	1	US-09-021-701-736	Sequence 736, App
C 743	15.4	0.2	17	1	US-08-484-138-23	Sequence 23, Appl	C 816	15.2	0.2	20	1	US-09-489-1750-13	Sequence 50, Appl
C 744	15.4	0.2	17	1	US-08-292-620A-1931	Sequence 1931, Ap	C 817	15.2	0.2	20	1	US-09-489-1765A-38	Sequence 38, Appl
C 745	15.4	0.2	17	1	US-09-071-845-1931	Sequence 1931, Ap	C 818	15.2	0.2	20	1	US-09-657-042A-38	Sequence 28, Appl
C 746	15.4	0.2	17	1	US-08-584-040-2884	Sequence 2884, Ap	C 819	15.2	0.2	20	1	US-09-651-011A-28	Sequence 9, Appl
C 747	15.4	0.2	17	1	US-09-371-772B-1408	Sequence 1408, Ap	C 820	15.2	0.2	20	1	US-09-536-259-9	Sequence 92, Appl
C 748	15.4	0.2	17	1	US-09-371-772B-5562	Sequence 5562, Ap	C 821	15.2	0.2	20	1	US-09-629-645A-92	Sequence 85, Appl
C 749	15.4	0.2	17	1	PCT-US95-06379-23	Sequence 23, Appl	C 822	15.2	0.2	20	1	US-09-659-791A-85	Sequence 19, Appl
C 750	15.4	0.2	18	1	US-09-140-804-18	Sequence 18, Appl	C 823	15.2	0.2	20	1	US-09-295-593-19	Sequence 104, Appl
C 751	15.4	0.2	18	1	US-09-686-838B-18	Sequence 18, Appl	C 824	15.2	0.2	20	1	US-09-676-610B-114	Sequence 40, Appl
C 752	15.4	0.2	18	1	US-09-435-019-48	Sequence 48, Appl	C 825	15.2	0.2	20	1	US-09-844-525A-45	Sequence 45, Appl
C 753	15.4	0.2	18	1	PCT-US91-03680-73	Sequence 73, Appl	C 826	15.2	0.2	20	1	US-09-725-265-40	Sequence 40, Appl
C 754	15.4	0.2	18	1	PCT-US91-03680-74	Sequence 74, Appl	C 827	15.2	0.2	20	1	US-09-725-265-41	Sequence 41, Appl
C 755	15.4	0.2	19	1	US-07-985-691-9	Sequence 9, Appl	C 828	15.2	0.2	20	1	US-09-920-759-88	Sequence 82, Appl
C 756	15.4	0.2	19	1	US-08-631-200-39	Sequence 39, Appl	C 829	15.2	0.2	20	1	US-09-060-299-289	Sequence 289, App
C 757	15.4	0.2	19	1	US-08-829-553-39	Sequence 39, Appl	C 830	15.2	0.2	20	1	US-09-402-923A-2391	Sequence 2391, App
C 758	15.4	0.2	19	1	US-08-923-267A-39	Sequence 39, Appl	C 831	15.2	0.2	20	1	US-09-198-452A-2978	Sequence 2978, Ap
C 759	15.4	0.2	19	1	US-08-936-707A-39	Sequence 39, Appl	C 832	15.2	0.2	20	1	US-09-198-452A-5002	Sequence 5002, Ap
C 760	15.4	0.2	19	1	US-08-936-706A-39	Sequence 39, Appl	C 833	15.2	0.2	20	1	US-09-198-452A-5002	Sequence 5002, Ap
C 761	15.4	0.2	19	1	US-09-248-203-39	Sequence 39, Appl	C 834	15.2	0.2	20	1	US-09-198-452A-5785	Sequence 5785, Ap
C 762	15.4	0.2	19	1	US-09-009-913-216	Sequence 216, App	C 835	15.2	0.2	20	1	US-09-198-452A-6476	Sequence 6476, Ap
C 763	15.4	0.2	19	1	US-09-406-071-39	Sequence 39, Appl	C 836	15.2	0.2	20	1	US-09-198-452A-6842	Sequence 6842, Ap

C 837	15.2	0.2	20	1	US-09-601-144-20	Sequence 20, Appl	910	15	0.2	15	1	US-09-071-845-362	Sequence 362, App
C 838	15.2	0.2	20	1	US-09-823-634A-18	Sequence 18, Appl	911	15	0.2	15	1	US-09-142-521-3	Sequence 3, Appl
C 839	15.2	0.2	20	1	US-09-823-647B-18	Sequence 18, Appl	911	15	0.2	15	1	US-09-142-521-5	Sequence 5, Appl
C 840	15.2	0.2	20	1	US-09-780-045-104	Sequence 104, Appl	C 913	15	0.2	15	1	US-09-167-775-1	Sequence 1, Appl
C 841	15.2	0.2	20	1	PCT-US94-02891-22	Sequence 22, Appl	C 914	15	0.2	15	1	US-08-150-156A-19	Sequence 19, Appl
C 842	15.2	0.2	21	1	US-08-145-704-11	Sequence 11, Appl	C 915	15	0.2	15	1	US-08-150-156A-20	Sequence 20, Appl
C 843	15.2	0.2	21	1	US-08-207-901-4	Sequence 4, Appl	C 916	15	0.2	15	1	US-08-108-591B-17	Sequence 17, Appl
C 844	15.2	0.2	21	1	US-08-639-501-57	Sequence 57, Appl	C 917	15	0.2	15	1	US-08-108-591B-18	Sequence 18, Appl
C 845	15.2	0.2	21	1	US-08-416-711-9	Sequence 9, Appl	C 918	15	0.2	15	1	US-09-619-103-21	Sequence 21, Appl
C 846	15.2	0.2	21	1	US-09-044-946-57	Sequence 57, Appl	C 919	15	0.2	15	1	US-09-300-588A-68	Sequence 68, Appl
C 847	15.2	0.2	21	1	US-09-044-908-57	Sequence 57, Appl	C 920	15	0.2	15	1	US-08-988-024C-9	Sequence 9, Appl
C 848	15.2	0.2	21	1	US-08-587-574-11	Sequence 11, Appl	C 921	15	0.2	15	1	US-09-435-739-5	Sequence 5, Appl
C 849	15.2	0.2	21	1	US-08-535-168-11	Sequence 11, Appl	C 922	15	0.2	15	1	US-10-091-231-2	Sequence 2, Appl
C 850	15.2	0.2	21	1	US-09-017-974-11	Sequence 11, Appl	C 923	15	0.2	15	1	US-09-930-218-5	Sequence 5, Appl
C 851	15.2	0.2	21	1	US-08-682-255A-11	Sequence 11, Appl	C 924	15	0.2	15	1	PCT-US91-03680-15	Sequence 15, Appl
C 852	15.2	0.2	21	1	US-09-429-130-11	Sequence 11, Appl	C 925	15	0.2	15	1	US-09-507-345A-3	Sequence 3, Appl
C 853	15.2	0.2	21	1	US-09-227-595-14	Sequence 14, Appl	C 926	15	0.2	15	1	US-09-507-345A-4	Sequence 4, Appl
C 854	15.2	0.2	21	1	US-09-356-497-9	Sequence 9, Appl	C 927	15	0.2	15	1	US-09-507-345A-5	Sequence 5, Appl
C 855	15.2	0.2	21	1	US-09-423-978-6964	Sequence 6964, Ap	C 928	15	0.2	15	1	US-09-507-345A-6	Sequence 6, Appl
C 856	15.2	0.2	21	1	US-09-422-978-6936	Sequence 9636, Ap	C 929	15	0.2	15	1	US-09-507-345A-7	Sequence 7, Appl
C 857	15.2	0.2	21	1	US-09-422-978-11166	Sequence 11166, A	C 930	15	0.2	15	1	US-09-507-345A-8	Sequence 8, Appl
C 858	15.2	0.2	21	1	PCT-US96-11786-11	Sequence 11, Appl	C 931	15	0.2	15	1	US-09-739-928-3	Sequence 3, Appl
C 859	15.2	0.2	22	1	US-08-457-273B-22	Sequence 22, Appl	C 932	15	0.2	15	1	US-09-739-928-4	Sequence 4, Appl
C 860	15.2	0.2	22	1	US-08-104-165-29	Sequence 29, Appl	C 933	15	0.2	15	1	US-09-739-928-5	Sequence 5, Appl
C 861	15.2	0.2	22	1	US-08-187-161-4	Sequence 4, Appl	C 934	15	0.2	15	1	US-09-739-928-6	Sequence 6, Appl
C 862	15.2	0.2	22	1	US-08-464-250-29	Sequence 29, Appl	C 935	15	0.2	15	1	US-09-739-928-7	Sequence 7, Appl
C 863	15.2	0.2	22	1	US-08-464-250-29	Sequence 29, Appl	C 936	15	0.2	15	1	US-09-739-928-8	Sequence 8, Appl
C 864	15.2	0.2	22	1	US-09-126-980-4	Sequence 4, Appl	C 937	15	0.2	15	1	US-08-584-940-2547	Sequence 2547, Ap
C 865	15.2	0.2	22	1	US-09-476-482-4	Sequence 4, Appl	C 938	15	0.2	15	1	US-08-584-940-2552	Sequence 2552, Ap
C 866	15.2	0.2	22	1	US-08-897-956A-23	Sequence 23, Appl	C 939	15	0.2	15	1	US-09-475-447A-118	Sequence 118, Ap
C 867	15.2	0.2	22	1	US-09-390-134B-13	Sequence 13, Appl	C 940	15	0.2	15	1	US-09-300-858A-63	Sequence 63, Appl
C 868	15.2	0.2	22	1	US-09-780-172-11	Sequence 11, Appl	C 941	15	0.2	15	1	US-09-371-772B-1071	Sequence 1071, Ap
C 869	15.2	0.2	22	1	US-09-445-283C-45	Sequence 45, Appl	C 942	15	0.2	15	1	US-09-371-772B-1076	Sequence 1076, Ap
C 870	15.2	0.2	22	1	US-09-750-401-17	Sequence 17, Appl	C 943	15	0.2	15	1	US-09-866-108A-1537	Sequence 1537, Ap
C 871	15.2	0.2	22	1	US-09-750-401-19	Sequence 19, Appl	C 944	15	0.2	15	1	US-09-866-108A-1538	Sequence 1538, Ap
C 872	15.2	0.2	23	1	US-08-061-539-1	Sequence 1, Appl	C 945	15	0.2	15	1	US-09-866-108A-1539	Sequence 1539, Ap
C 873	15.2	0.2	23	1	US-08-466-647-1	Sequence 1, Appl	C 946	15	0.2	15	1	US-09-487-444-11	Sequence 11, Appl
C 874	15.2	0.2	23	1	US-08-411-795B-1	Sequence 1, Appl	C 947	15	0.2	15	1	US-09-437-076-1	Sequence 1, Appl
C 875	15.2	0.2	23	1	US-08-411-796-1	Sequence 1, Appl	C 948	15	0.2	15	1	US-09-437-076-2	Sequence 2, Appl
C 876	15.2	0.2	23	1	US-08-469-319A-1	Sequence 1, Appl	C 949	15	0.2	15	1	US-09-349-035-2	Sequence 2, Appl
C 877	15.2	0.2	23	1	US-08-378-617A-6	Sequence 6, Appl	C 950	15	0.2	15	1	US-09-593-359-9	Sequence 9, Appl
C 878	15.2	0.2	23	1	US-08-837-302-6	Sequence 6, Appl	C 951	15	0.2	15	1	US-08-715-461-3	Sequence 3, Appl
C 879	15.2	0.2	23	1	US-08-798-668-6	Sequence 6, Appl	C 952	15	0.2	15	1	US-08-715-461-4	Sequence 4, Appl
C 880	15.2	0.2	23	1	US-08-471-039-1	Sequence 1, Appl	C 953	15	0.2	15	1	US-09-209-368-63	Sequence 63, Appl
C 881	15.2	0.2	23	1	US-08-855-825-6	Sequence 6, Appl	C 954	15	0.2	15	1	US-09-844-634-57	Sequence 57, Appl
C 882	15.2	0.2	23	1	US-09-395-345-24	Sequence 24, Appl	C 955	15	0.2	15	1	US-09-389-956-87	Sequence 87, Appl
C 883	15.2	0.2	23	1	US-08-764-114-1	Sequence 1, Appl	C 956	15	0.2	15	1	US-09-860-473-142	Sequence 142, App
C 884	15.2	0.2	23	1	US-09-091-952A-39	Sequence 39, Appl	C 957	15	0.2	15	1	US-09-422-978-9155	Sequence 9155, Ap
C 885	15.2	0.2	23	1	US-08-469-419-1	Sequence 1, Appl	C 958	15	0.2	15	1	US-07-918-318-19	Sequence 19, Appl
C 886	15.2	0.2	23	1	US-08-559-330-1	Sequence 1, Appl	C 959	15	0.2	15	1	US-08-242-402-6	Sequence 6, Appl
C 887	15.2	0.2	23	1	US-09-419-406-6	Sequence 6, Appl	C 960	15	0.2	15	1	US-08-270-180-17	Sequence 17, Appl
C 888	15.2	0.2	23	1	PCT-US93-11198-1	Sequence 1, Appl	C 961	15	0.2	15	1	US-08-295-643-22	Sequence 22, Appl
C 889	15.2	0.2	29	1	US-08-666-405-15	Sequence 15, Appl	C 962	15	0.2	15	1	US-08-682-423-17	Sequence 17, Appl
C 890	15.2	0.2	36	1	US-08-863-639A-31	Sequence 31, Appl	C 963	15	0.2	15	1	US-08-682-423-29	Sequence 29, Appl
C 891	15	0.2	15	1	US-08-452-196A-6	Sequence 6, Appl	C 964	15	0.2	15	1	US-09-359-756-2	Sequence 2, Appl
C 892	15	0.2	15	1	US-07-971-978-1	Sequence 1, Appl	C 965	15	0.2	15	1	US-09-230-704-3	Sequence 3, Appl
C 893	15	0.2	15	1	US-08-756-728A-2	Sequence 2, Appl	C 966	15	0.2	15	1	US-09-609-162-3	Sequence 3, Appl
C 894	15	0.2	15	1	US-08-663-918-3	Sequence 3, Appl	C 967	15	0.2	15	1	US-09-634-732-3	Sequence 3, Appl
C 895	15	0.2	15	1	US-08-663-918-4	Sequence 4, Appl	C 968	15	0.2	15	1	US-09-597-771-23	Sequence 23, Appl
C 896	15	0.2	15	1	US-08-292-620A-361	Sequence 361, App	C 969	15	0.2	15	1	US-09-180-245-67	Sequence 67, Appl
C 897	15	0.2	15	1	US-08-771-789-3	Sequence 3, Appl	C 970	15	0.2	15	1	US-09-364-425B-33	Sequence 33, Appl
C 898	15	0.2	15	1	US-08-771-789-4	Sequence 4, Appl	C 971	15	0.2	15	1	US-09-860-473-13	Sequence 13, Appl
C 899	15	0.2	15	1	US-08-358-556A-10	Sequence 10, Appl	C 972	15	0.2	15	1	PCT-US95-05141-17	Sequence 17, Appl
C 900	15	0.2	15	1	US-08-358-556A-16	Sequence 16, Appl	C 973	15	0.2	15	1	PCT-US95-05141-29	Sequence 29, Appl
C 901	15	0.2	15	1	US-08-922-170B-5	Sequence 5, Appl	C 974	15	0.2	15	1	US-09-475-947A-114	Sequence 114, App
C 902	15	0.2	15	1	US-08-863-639A-5	Sequence 5, Appl	C 975	15	0.2	15	1	US-09-356-806-82	Sequence 82, Appl
C 903	15	0.2	15	1	US-08-863-639A-7	Sequence 7, Appl	C 976	15	0.2	15	1	US-08-621-914A-2	Sequence 2, Appl
C 904	15	0.2	15	1	US-08-863-639A-9	Sequence 9, Appl	C 977	15	0.2	15	1	US-08-873-437-2	Sequence 2, Appl
C 905	15	0.2	15	1	US-08-863-639A-1	Sequence 1, Appl	C 978	15	0.2	15	1	US-09-522-217-39	Sequence 39, Appl
C 906	15	0.2	15	1	US-08-693-831-1	Sequence 1, Appl	C 979	15	0.2	15	1	US-09-593-312-2	Sequence 2, Appl
C 907	15	0.2	15	1	US-08-832-021-62	Sequence 62, Appl	C 980	15	0.2	15	1	US-09-923-246-39	Sequence 39, Appl
C 908	15	0.2	15	1	US-09-183-619-4	Sequence 4, Appl	C 981	15	0.2	15	1	US-09-658-077-1	Sequence 1, Appl
C 909	15	0.2	15	1	US-09-071-845-361	Sequence 361, App	C 982	15	0.2	15	1	US-10-295-723-39	Sequence 39, Appl



983	15	0.2	29	1	US-10-003-998A-7	Sequence 7, Appl	1056	14.8	0.2	20	1	US-09-485-077A-3	Sequence 3, Appl
984	14.8	0.2	18	1	US-08-152-113-80	Sequence 80, Appl	c1057	14.8	0.2	20	1	US-09-725-265-36	Sequence 36, Appl
985	14.8	0.2	18	1	US-08-330-000-1	Sequence 80, Appl	c1058	14.8	0.2	20	1	US-09-725-265-42	Sequence 42, Appl
986	14.8	0.2	18	1	US-08-579-223-80	Sequence 80, Appl	c1059	14.8	0.2	20	1	US-09-422-978-7819	Sequence 7819, Ap
C 987	14.8	0.2	18	1	US-08-487-046-5	Sequence 5, Appl	1060	14.8	0.2	20	1	US-09-060-299-288	Sequence 288, App
C 988	14.8	0.2	18	1	US-08-487-046-6	Sequence 6, Appl	1061	14.8	0.2	20	1	US-09-402-922A-288	Sequence 288, App
C 989	14.8	0.2	18	1	US-08-483-522-5	Sequence 5, Appl	1062	14.8	0.2	20	1	US-09-198-452A-4204	Sequence 4204, Ap
990	14.8	0.2	18	1	US-08-483-522-6	Sequence 6, Appl	1063	14.8	0.2	20	1	US-09-254-778B-28	Sequence 28, Appl
991	14.8	0.2	18	1	US-09-213-768-17	Sequence 17, Appl	1064	14.8	0.2	20	1	US-09-249-247-158	Sequence 158, App
992	14.8	0.2	18	1	US-09-106-038A-24	Sequence 24, Appl	c1065	14.8	0.2	20	1	US-09-526-193A-150	Sequence 150, App
993	14.8	0.2	18	1	US-08-965-908-1	Sequence 1, Appl	1066	14.8	0.2	20	1	US-09-980-052-146	Sequence 146, App
C 994	14.8	0.2	18	1	US-09-344-579-35	Sequence 35, Appl	c1067	14.8	0.2	20	1	5185441-9	Sequence 46, Appl
C 995	14.8	0.2	18	1	US-09-199-859-36	Sequence 36, Appl	1068	14.8	0.2	20	1	5185441-11	Sequence 46, Appl
C 996	14.8	0.2	18	1	US-08-679-645-1169	Sequence 1169, Ap	1069	14.8	0.2	21	1	US-07-977-284A-62	Sequence 62, Appl
C 997	14.8	0.2	18	1	US-08-275-951-32	Sequence 32, Appl	c1070	14.8	0.2	21	1	US-08-498-402-4	Sequence 4, Appl
C 998	14.8	0.2	18	1	US-08-275-951-32	Sequence 32, Appl	c1071	14.8	0.2	21	1	US-08-451-777A-10	Sequence 10, Appl
999	14.8	0.2	18	1	US-08-275-951-33	Sequence 33, Appl	c1072	14.8	0.2	21	1	US-08-451-778A-10	Sequence 10, Appl
1000	14.8	0.2	18	1	US-09-475-947A-340	Sequence 340, App	c1073	14.8	0.2	21	1	US-08-998-208-10	Sequence 10, Appl
c1001	14.8	0.2	18	1	US-09-280-030-28	Sequence 28, Appl	1074	14.8	0.2	21	1	US-08-460-751-17	Sequence 17, Appl
c1002	14.8	0.2	18	1	US-09-422-978-6054	Sequence 6054, Ap	1075	14.8	0.2	21	1	US-08-256-426B-62	Sequence 62, Appl
c1003	14.8	0.2	18	1	US-09-422-978-11203	Sequence 11203, A	1076	14.8	0.2	21	1	US-08-193-627-10	Sequence 10, Appl
c1004	14.8	0.2	18	1	US-09-856-747-46	Sequence 46, Appl	1077	14.8	0.2	21	1	US-09-347-114A-9	Sequence 9, Appl
c1005	14.8	0.2	18	1	PCT-US94-12947A-80	Sequence 80, Appl	1078	14.8	0.2	21	1	US-09-081-142-12	Sequence 12, Appl
c1006	14.8	0.2	19	1	US-08-167-113-8	Sequence 8, Appl	c1079	14.8	0.2	21	1	US-09-598-747-21	Sequence 21, Appl
c1007	14.8	0.2	19	1	US-08-886-161-8	Sequence 8, Appl	1080	14.8	0.2	21	1	US-09-422-978-7056	Sequence 7056, Ap
1008	14.8	0.2	19	1	US-08-899-029-1	Sequence 1, Appl	c1081	14.8	0.2	21	1	US-09-065-040-6	Sequence 6, Appl
1009	14.8	0.2	19	1	US-09-422-978-5817	Sequence 5817, Ap	c1082	14.8	0.2	21	1	US-09-546-986A-12	Sequence 12, Appl
1010	14.8	0.2	20	1	US-08-502-185-27	Sequence 27, Appl	c1083	14.8	0.2	21	1	US-09-524-730-12	Sequence 12, Appl
1011	14.8	0.2	20	1	US-08-502-185-34	Sequence 34, Appl	1084	14.8	0.2	21	1	US-09-435-773-17	Sequence 17, Appl
1012	14.8	0.2	20	1	US-08-502-185-37	Sequence 34, Appl	c1085	14.8	0.2	21	1	PCT-US95-06733-10	Sequence 10, Appl
1013	14.8	0.2	20	1	US-08-398-945-37	Sequence 37, Appl	c1086	14.8	0.2	21	1	PCT-US95-10721-4	Sequence 4, Appl
1014	14.8	0.2	20	1	US-08-398-945-27	Sequence 34, Appl	1087	14.8	0.2	22	1	US-08-457-277B-31	Sequence 31, Appl
1015	14.8	0.2	20	1	US-08-398-945-37	Sequence 37, Appl	1088	14.8	0.2	22	1	US-09-068-109-3	Sequence 3, Appl
c1016	14.8	0.2	20	1	US-08-371-121-19	Sequence 19, Appl	c1089	14.8	0.2	22	1	US-08-538-666-14	Sequence 14, Appl
1017	14.8	0.2	20	1	US-08-501-779-27	Sequence 27, Appl	c1090	14.8	0.2	22	1	US-08-538-666-20	Sequence 20, Appl
1018	14.8	0.2	20	1	US-08-501-779-34	Sequence 34, Appl	c1091	14.8	0.2	22	1	US-09-183-412-52	Sequence 52, Appl
1019	14.8	0.2	20	1	US-08-501-779-37	Sequence 37, Appl	1092	14.8	0.2	22	1	US-09-245-041-50	Sequence 50, Appl
1020	14.8	0.2	20	1	US-08-501-713-27	Sequence 27, Appl	c1093	14.8	0.2	22	1	US-09-769-864-52	Sequence 52, Appl
1021	14.8	0.2	20	1	US-08-501-713-34	Sequence 34, Appl	c1094	14.8	0.2	22	1	US-09-688-990-20	Sequence 20, Appl
1022	14.8	0.2	20	1	US-08-501-713-37	Sequence 37, Appl	c1095	14.8	0.2	26	1	US-08-621-914A-1	Sequence 1, Appl
1023	14.8	0.2	20	1	US-08-378-860-27	Sequence 27, Appl	c1096	14.8	0.2	26	1	US-09-197-951-5	Sequence 5, Appl
1024	14.8	0.2	20	1	US-08-378-860-34	Sequence 34, Appl	c1097	14.8	0.2	26	1	US-09-522-921-38	Sequence 38, Appl
1025	14.8	0.2	20	1	US-08-378-860-37	Sequence 37, Appl	c1098	14.8	0.2	26	1	US-09-527-346-7	Sequence 7, Appl
1026	14.8	0.2	20	1	US-08-501-626-27	Sequence 27, Appl	c1099	14.8	0.2	26	1	US-09-923-246-38	Sequence 38, Appl
1027	14.8	0.2	20	1	US-08-501-626-34	Sequence 34, Appl	c1100	14.8	0.2	26	1	US-10-295-723-38	Sequence 38, Appl
1028	14.8	0.2	20	1	US-08-501-626-37	Sequence 37, Appl	1101	14.8	0.2	28	1	US-08-762-106-11	Sequence 11, Appl
1029	14.8	0.2	20	1	US-08-501-356-27	Sequence 27, Appl	1102	14.8	0.2	28	1	US-09-320-774-11	Sequence 11, Appl
1030	14.8	0.2	20	1	US-08-501-356-34	Sequence 34, Appl	1103	14.6	0.2	21	1	US-08-146-504-2	Sequence 2, Appl
1031	14.8	0.2	20	1	US-08-501-356-37	Sequence 37, Appl	1104	14.6	0.2	21	1	US-08-725-976-2	Sequence 2, Appl
c1032	14.8	0.2	20	1	US-08-237-180B-46	Sequence 46, Appl	1105	14.6	0.2	21	1	US-08-271-882B-2	Sequence 2, Appl
c1033	14.8	0.2	20	1	US-08-692-787-62	Sequence 62, Appl	1106	14.6	0.2	21	1	US-08-726-278-2	Sequence 2, Appl
c1034	14.8	0.2	20	1	US-08-837-201C-97	Sequence 97, Appl	c1107	14.6	0.2	21	1	US-08-009-263C-52	Sequence 52, Appl
1035	14.8	0.2	20	1	US-08-904-901-158	Sequence 158, App	1108	14.6	0.2	21	1	US-08-128-011-4	Sequence 4, Appl
c1036	14.8	0.2	20	1	US-07-927-391-20	Sequence 20, Appl	1109	14.6	0.2	21	1	US-07-847-055A-12	Sequence 12, Appl
c1037	14.8	0.2	20	1	US-08-940-250-24	Sequence 24, Appl	c1110	14.6	0.2	21	1	US-08-202-389-44	Sequence 44, Appl
c1038	14.8	0.2	20	1	US-08-858-876A-6	Sequence 6, Appl	c1111	14.6	0.2	21	1	US-08-426-792-2	Sequence 2, Appl
1039	14.8	0.2	20	1	US-09-357-070-24	Sequence 24, Appl	c1112	14.6	0.2	21	1	US-08-424-663-4	Sequence 4, Appl
1040	14.8	0.2	20	1	US-09-249-730-158	Sequence 158, App	c1113	14.6	0.2	21	1	US-08-424-663-5	Sequence 5, Appl
1041	14.8	0.2	20	1	US-09-418-641-75	Sequence 75, Appl	c1114	14.6	0.2	21	1	US-08-647-351B-2	Sequence 2, Appl
c1042	14.8	0.2	20	1	US-09-280-799-28	Sequence 28, Appl	c1115	14.6	0.2	21	1	US-08-740-215B-4	Sequence 4, Appl
c1043	14.8	0.2	20	1	US-09-517-584A-78	Sequence 78, Appl	1116	14.6	0.2	21	1	US-08-740-215B-1	Sequence 1, Appl
c1044	14.8	0.2	20	1	US-09-101-886B-77	Sequence 77, Appl	1117	14.6	0.2	21	1	US-08-403-888A-63	Sequence 63, Appl
c1045	14.8	0.2	20	1	US-09-097-199-62	Sequence 77, Appl	1118	14.6	0.2	21	1	US-08-403-888A-142	Sequence 142, App
1046	14.8	0.2	20	1	US-09-021-701-735	Sequence 735, App	c1119	14.6	0.2	21	1	US-08-872-446-4	Sequence 4, Appl
c1047	14.8	0.2	20	1	US-09-593-711A-152	Sequence 152, App	c1120	14.6	0.2	21	1	US-08-872-446-5	Sequence 5, Appl
c1048	14.8	0.2	20	1	US-09-472-880-6	Sequence 6, Appl	c1121	14.6	0.2	21	1	US-08-838-718B-52	Sequence 52, Appl
1049	14.8	0.2	20	1	US-09-364-416-97	Sequence 97, Appl	1122	14.6	0.2	21	1	US-08-974-549A-507	Sequence 507, App
1050	14.8	0.2	20	1	US-09-468-872-79	Sequence 79, Appl	c1123	14.6	0.2	21	1	US-08-943-731-256	Sequence 256, App
c1051	14.8	0.2	20	1	US-09-629-645A-159	Sequence 159, App	1124	14.6	0.2	21	1	US-09-109-663-14	Sequence 14, Appl
1052	14.8	0.2	20	1	US-09-561-497-87	Sequence 87, Appl	c1125	14.6	0.2	21	1	US-09-280-270A-4	Sequence 4, Appl
c1053	14.8	0.2	20	1	US-09-470-443-21	Sequence 21, Appl	c1126	14.6	0.2	21	1	US-09-280-270A-5	Sequence 5, Appl
1054	14.8	0.2	20	1	US-08-275-951-39	Sequence 39, Appl	c1127	14.6	0.2	21	1	US-09-270-542-96	Sequence 96, Appl
1055	14.8	0.2	20	1	US-08-275-951-48	Sequence 48, Appl	c1128	14.6	0.2	21	1	US-08-918-148-9	Sequence 9, Appl



c1129	14.6	0.2	21	1	US-09-031-962D-7	Sequence 7, Appli	1202	14.4	0.2	17	1	US-08-584-040-2741	Sequence 2741, Ap
c1130	14.6	0.2	21	1	US-08-912-951-274	Sequence 274, App	c1203	14.4	0.2	17	1	US-08-584-040-2885	Sequence 2885, Ap
c1131	14.6	0.2	21	1	US-09-187-288-11	Sequence 11, Appl	c1204	14.4	0.2	17	1	US-09-142-791A-7	Sequence 7, Appl1
c1132	14.6	0.2	21	1	US-09-187-288-12	Sequence 12, Appl	c1205	14.4	0.2	17	1	US-09-371-772B-1264	Sequence 1264, Ap
c1133	14.6	0.2	21	1	US-09-255-518C-9	Sequence 9, Appl1	c1206	14.4	0.2	17	1	US-09-371-772B-1265	Sequence 1265, Ap
c1134	14.6	0.2	21	1	US-09-422-978-6532	Sequence 6532, Ap	c1207	14.4	0.2	17	1	US-09-371-772B-1409	Sequence 1409, Ap
c1135	14.6	0.2	21	1	US-09-422-978-8263	Sequence 8263, Ap	c1208	14.4	0.2	17	1	US-09-866-108A-2192	Sequence 2192, Ap
c1136	14.6	0.2	21	1	US-09-422-978-10094	Sequence 10094, A	c1209	14.4	0.2	17	1	US-09-866-108A-2193	Sequence 2193, Ap
c1137	14.6	0.2	21	1	US-09-422-978-10129	Sequence 10129, A	c1210	14.4	0.2	17	1	US-09-866-108A-2668	Sequence 2668, Ap
c1138	14.6	0.2	21	1	US-09-422-978-10387	Sequence 10387, A	c1211	14.4	0.2	17	1	US-09-866-108A-2669	Sequence 2669, Ap
c1139	14.6	0.2	21	1	US-09-422-978-11222	Sequence 11222, A	c1212	14.4	0.2	17	1	US-09-866-108A-7981	Sequence 7981, Ap
c1140	14.6	0.2	21	1	US-09-402-181B-507	Sequence 507, App	c1213	14.4	0.2	17	1	US-09-866-108A-7982	Sequence 7982, Ap
c1141	14.6	0.2	21	1	US-09-721-456-507	Sequence 507, App	c1214	14.4	0.2	18	1	US-08-488-212A-51	Sequence 51, Appl
c1142	14.6	0.2	22	1	US-08-474-140-5	Sequence 5, Appl1	c1215	14.4	0.2	18	1	US-08-363-585-75	Sequence 75, Appl
c1143	14.6	0.2	22	1	US-08-477-630-5	Sequence 5, Appl1	c1216	14.4	0.2	18	1	US-08-358-995-18	Sequence 18, Appl
c1144	14.6	0.2	22	1	US-08-472-293-5	Sequence 5, Appl1	c1217	14.4	0.2	18	1	US-08-224-657-81	Sequence 81, Appl
c1145	14.6	0.2	22	1	US-08-474-545-5	Sequence 5, Appl1	c1218	14.4	0.2	18	1	US-08-758-978-979	Sequence 979, App
c1146	14.6	0.2	22	1	US-08-358-995-22	Sequence 22, Appl	c1219	14.4	0.2	18	1	US-08-653-037A-13	Sequence 13, Appl
c1147	14.6	0.2	22	1	US-08-753-147-9	Sequence 9, Appl1	c1220	14.4	0.2	18	1	US-08-117-952-425	Sequence 425, App
c1148	14.6	0.2	22	1	US-08-478-341-5	Sequence 5, Appl1	c1221	14.4	0.2	18	1	US-08-320-306-51	Sequence 51, Appl
c1149	14.6	0.2	22	1	US-08-465-590-121	Sequence 121, App	c1222	14.4	0.2	18	1	US-08-488-209B-51	Sequence 51, Appl
c1150	14.6	0.2	22	1	US-08-457-273B-30	Sequence 30, Appl	c1223	14.4	0.2	18	1	US-08-408-011-51	Sequence 51, Appl
c1151	14.6	0.2	22	1	US-08-910-484-4	Sequence 4, Appl1	c1224	14.4	0.2	18	1	US-08-389-423-28	Sequence 28, Appl
c1152	14.6	0.2	22	1	US-08-766-982-8	Sequence 8, Appl1	c1225	14.4	0.2	18	1	US-08-675-566-57	Sequence 57, Appl
c1153	14.6	0.2	22	1	US-08-962-790-2	Sequence 2, Appl1	c1226	14.4	0.2	18	1	US-09-280-409-15	Sequence 35, Appl
c1154	14.6	0.2	22	1	US-08-996-733-5	Sequence 5, Appl1	c1227	14.4	0.2	18	1	US-09-630-706-61	Sequence 61, Appl
c1155	14.6	0.2	22	1	US-08-781-891-81	Sequence 81, Appl	c1228	14.4	0.2	18	1	US-09-354-138-81	Sequence 81, Appl
c1156	14.6	0.2	22	1	US-08-781-891-88	Sequence 88, Appl	c1229	14.4	0.2	18	1	US-09-189-028-28	Sequence 28, Appl
c1157	14.6	0.2	22	1	US-09-010-641-5	Sequence 5, Appl1	c1230	14.4	0.2	18	1	US-09-920-760-43	Sequence 43, Appl
c1158	14.6	0.2	22	1	US-09-147-923-7	Sequence 7, Appl1	c1231	14.4	0.2	18	1	US-09-422-978-4233	Sequence 4233, Ap
c1159	14.6	0.2	22	1	US-08-275-526C-19	Sequence 19, Appl	c1232	14.4	0.2	18	1	US-09-422-978-5292	Sequence 5292, Ap
c1160	14.6	0.2	22	1	US-08-927-219-64	Sequence 64, Appl	c1233	14.4	0.2	18	1	US-09-422-978-5959	Sequence 5959, Ap
c1161	14.6	0.2	22	1	US-09-356-281-5	Sequence 5, Appl1	c1234	14.4	0.2	18	1	US-09-422-978-11161	Sequence 11161, A
c1162	14.6	0.2	22	1	US-08-711-417C-121	Sequence 121, App	c1235	14.4	0.2	19	1	US-08-967-101-171	Sequence 171, App
c1163	14.6	0.2	22	1	US-09-018-584A-95	Sequence 95, Appl	c1236	14.4	0.2	19	1	US-08-592-541-171	Sequence 171, App
c1164	14.6	0.2	22	1	US-09-296-219-8	Sequence 8, Appl1	c1237	14.4	0.2	19	1	US-09-124-698-171	Sequence 171, App
c1165	14.6	0.2	22	1	US-09-277-078-21	Sequence 21, Appl	c1238	14.4	0.2	19	1	US-09-135-698-171	Sequence 67, Appl
c1166	14.6	0.2	22	1	US-08-481-659C-20	Sequence 20, Appl	c1239	14.4	0.2	19	1	US-09-127-480-171	Sequence 171, App
c1167	14.6	0.2	22	1	US-09-383-316-108	Sequence 108, App	c1240	14.4	0.2	19	1	US-09-338-907-418	Sequence 418, App
c1168	14.6	0.2	22	1	US-09-462-569B-3	Sequence 3, Appl1	c1241	14.4	0.2	19	1	US-09-135-020-69	Sequence 69, Appl
c1169	14.6	0.2	22	1	US-09-076-677-19	Sequence 19, Appl	c1242	14.4	0.2	19	1	US-09-135-010A-69	Sequence 69, Appl
c1170	14.6	0.2	22	1	US-09-073-055-19	Sequence 19, Appl	c1243	14.4	0.2	19	1	US-09-444-471-69	Sequence 69, Appl
c1171	14.6	0.2	22	1	US-09-673-809-10	Sequence 10, Appl	c1244	14.4	0.2	19	1	US-09-218-207-418	Sequence 418, App
c1172	14.6	0.2	22	1	US-09-589-462-7	Sequence 7, Appl1	c1245	14.4	0.2	19	1	US-08-124-523-171	Sequence 171, App
c1173	14.6	0.2	22	1	US-09-454-495-7	Sequence 7, Appl1	c1246	14.4	0.2	19	1	US-09-345-882-117	Sequence 117, App
c1174	14.6	0.2	22	1	US-09-618-166-81	Sequence 81, Appl	c1247	14.4	0.2	19	1	US-09-597-735-69	Sequence 69, Appl
c1175	14.6	0.2	22	1	US-09-618-166-88	Sequence 88, Appl	c1248	14.4	0.2	19	1	US-09-444-295-69	Sequence 69, Appl
c1176	14.6	0.2	22	1	US-09-168-947-46	Sequence 46, Appl	c1249	14.4	0.2	19	1	US-09-597-732-69	Sequence 69, Appl
c1177	14.6	0.2	22	1	US-09-180-245-35	Sequence 25, Appl	c1250	14.4	0.2	19	1	US-09-636-796A-171	Sequence 171, App
c1178	14.6	0.2	22	1	US-09-180-245-27	Sequence 27, Appl	c1251	14.4	0.2	19	1	US-09-422-978-5006	Sequence 5006, App
c1179	14.6	0.2	22	1	US-09-180-245-29	Sequence 29, Appl	c1252	14.4	0.2	19	1	US-09-422-978-6457	Sequence 6457, Ap
c1180	14.6	0.2	22	1	US-09-180-245-31	Sequence 31, Appl	c1253	14.4	0.2	19	1	US-09-422-978-8352	Sequence 8352, Ap
c1181	14.6	0.2	22	1	US-09-180-245-33	Sequence 33, Appl	c1254	14.4	0.2	19	1	US-09-060-299-54	Sequence 54, Appl
c1182	14.6	0.2	22	1	US-09-180-245-35	Sequence 35, Appl	c1255	14.4	0.2	19	1	US-09-402-923A-54	Sequence 54, Appl
c1183	14.6	0.2	22	1	US-09-180-245-37	Sequence 37, Appl	c1256	14.4	0.2	19	1	US-09-597-731-69	Sequence 69, Appl
c1184	14.6	0.2	22	1	US-09-723-909-121	Sequence 121, App	c1257	14.4	0.2	20	1	US-08-317-648-3	Sequence 3, Appl1
c1185	14.6	0.2	22	1	PCT-US93-08743-121	Sequence 121, App	c1258	14.4	0.2	20	1	US-08-502-185-13	Sequence 13, Appl
c1186	14.6	0.2	25	1	US-09-866-108A-13467	Sequence 2, Appl1	c1259	14.4	0.2	20	1	US-08-398-945-12	Sequence 12, Appl
c1187	14.6	0.2	30	1	US-08-771-781-2	Sequence 70, Appl	c1260	14.4	0.2	20	1	US-08-501-779-12	Sequence 12, Appl
c1188	14.4	0.2	16	1	US-09-479-005A-70	Sequence 76, App	c1261	14.4	0.2	20	1	US-08-376-162A-8	Sequence 8, Appl1
c1189	14.4	0.2	17	1	US-08-373-124A-736	Sequence 972, App	c1262	14.4	0.2	20	1	US-08-501-713-13	Sequence 13, Appl
c1190	14.4	0.2	17	1	US-08-373-124A-1965	Sequence 972, App	c1263	14.4	0.2	20	1	US-08-588-821-71	Sequence 71, Appl
c1191	14.4	0.2	17	1	US-08-373-124A-2053	Sequence 1965, Ap	c1264	14.4	0.2	20	1	US-08-378-860-12	Sequence 12, Appl
c1193	14.4	0.2	17	1	US-08-373-124A-2143	Sequence 2053, Ap	c1265	14.4	0.2	20	1	US-08-217-082A-3	Sequence 3, Appl1
c1194	14.4	0.2	17	1	US-08-373-124A-2145	Sequence 2143, Ap	c1266	14.4	0.2	20	1	US-08-501-826-12	Sequence 12, Appl
c1195	14.4	0.2	17	1	US-08-435-628-736	Sequence 2145, Ap	c1267	14.4	0.2	20	1	US-08-915-214-71	Sequence 71, Appl
c1196	14.4	0.2	17	1	US-08-435-628-972	Sequence 736, App	c1268	14.4	0.2	20	1	US-08-501-356-12	Sequence 12, Appl
c1197	14.4	0.2	17	1	US-08-435-628-1965	Sequence 972, App	c1269	14.4	0.2	20	1	US-08-465-885A-3	Sequence 32, Appl1
c1198	14.4	0.2	17	1	US-08-435-628-2053	Sequence 1965, Ap	c1270	14.4	0.2	20	1	US-08-229-528-32	Sequence 32, Appl
c1199	14.4	0.2	17	1	US-08-435-628-2143	Sequence 2053, Ap	c1271	14.4	0.2	20	1	US-09-005-532-71	Sequence 71, Appl
c1200	14.4	0.2	17	1	US-08-435-628-2145	Sequence 2143, Ap	c1272	14.4	0.2	20	1	US-09-080-285-3	Sequence 3, Appl1
c1201	14.4	0.2	17	1	US-08-584-040-2740	Sequence 2145, Ap	c1273	14.4	0.2	20	1	US-08-987-326-12	Sequence 12, Appl
			17	1		Sequence 2740, Ap	c1274	14.4	0.2	20	1	US-09-166-186-6221	Sequence 221, App

c1275	14.4	0.2	20	1	US-08-882-046-74	Sequence 74, Appl	1348	14.2	0.2	16	1	US-08-882-649A-8	Sequence 8, Appl1
1276	14.4	0.2	20	1	US-09-286-904-76	Sequence 76, Appl	c1349	14.2	0.2	19	1	US-08-701-380-5	Sequence 5, Appl1
c1277	14.4	0.2	20	1	US-09-429-323-78	Sequence 78, Appl	1350	14.2	0.2	19	1	US-08-851-135-1	Sequence 1, Appl1
1278	14.4	0.2	20	1	US-08-765-340-26	Sequence 26, Appl	1351	14.2	0.2	19	1	US-08-996-306-46	Sequence 46, Appl
c1279	14.4	0.2	20	1	US-09-359-756-31	Sequence 31, Appl	1352	14.2	0.2	19	1	US-08-832-078-3	Sequence 3, Appl1
c1280	14.4	0.2	20	1	US-09-435-296-26	Sequence 26, Appl	c1353	14.2	0.2	19	1	US-09-032-365A-39	Sequence 39, Appl1
c1281	14.4	0.2	20	1	US-09-358-683-26	Sequence 26, Appl	1354	14.2	0.2	19	1	US-09-338-907-46	Sequence 46, Appl
c1282	14.4	0.2	20	1	US-09-313-932-221	Sequence 221, App	1355	14.2	0.2	19	1	US-09-338-907-380	Sequence 380, App
c1283	14.4	0.2	20	1	US-09-313-932-366	Sequence 366, App	1356	14.2	0.2	19	1	US-09-218-207-46	Sequence 46, Appl
1284	14.4	0.2	20	1	US-09-021-701-727	Sequence 727, App	1357	14.2	0.2	19	1	US-09-218-207-380	Sequence 380, App
1285	14.4	0.2	20	1	US-08-906-156A-87	Sequence 87, Appl	c1358	14.2	0.2	19	1	US-09-531-000-21	Sequence 21, Appl
c1286	14.4	0.2	20	1	US-09-489-765A-25	Sequence 25, Appl	c1359	14.2	0.2	19	1	US-09-422-978-4116	Sequence 4116, Ap
c1287	14.4	0.2	20	1	US-09-489-765A-25	Sequence 25, Appl	c1360	14.2	0.2	19	1	US-09-422-978-6486	Sequence 6486, Ap
c1288	14.4	0.2	20	1	US-09-798-096-67	Sequence 67, Appl	1361	14.2	0.2	19	1	US-09-422-978-7856	Sequence 7856, Ap
1289	14.4	0.2	20	1	US-09-724-426-3	Sequence 3, Appl1	c1362	14.2	0.2	19	1	US-09-422-978-11738	Sequence 11738, A
1290	14.4	0.2	20	1	US-09-658-679A-50	Sequence 50, Appl	1363	14.2	0.2	20	1	US-08-108-591B-4	Sequence 4, Appl1
1291	14.4	0.2	20	1	US-09-658-679A-51	Sequence 51, Appl	c1364	14.2	0.2	20	1	US-07-952-442-21	Sequence 21, Appl
c1292	14.4	0.2	20	1	US-09-640-101-76	Sequence 76, Appl	1365	14.2	0.2	20	1	US-08-138-608-53	Sequence 53, Appl
c1293	14.4	0.2	20	1	US-08-626-285-48	Sequence 48, Appl	1366	14.2	0.2	20	1	US-07-984-04A-8	Sequence 8, Appl1
1294	14.4	0.2	20	1	US-09-668-313A-118	Sequence 118, App	c1367	14.2	0.2	20	1	US-08-142-845-12	Sequence 12, Appl
1295	14.4	0.2	20	1	US-09-422-978-5670	Sequence 5670, Ap	1368	14.2	0.2	20	1	US-08-142-845-16	Sequence 16, Appl
1296	14.4	0.2	20	1	US-09-422-978-9656	Sequence 9656, Ap	1369	14.2	0.2	20	1	US-08-117-328-4	Sequence 4, Appl1
c1297	14.4	0.2	20	1	US-09-973-959-2	Sequence 2, Appl1	c1370	14.2	0.2	20	1	US-08-250-856A-28	Sequence 28, Appl
c1298	14.4	0.2	20	1	US-09-705-267A-152	Sequence 152, App	c1371	14.2	0.2	20	1	US-08-179-738-22	Sequence 22, Appl
c1299	14.4	0.2	20	1	US-09-198-452A-1513	Sequence 1513, Ap	1372	14.2	0.2	20	1	US-08-222-177A-240	Sequence 240, App
c1300	14.4	0.2	20	1	US-09-198-452A-1915	Sequence 1915, Ap	c1373	14.2	0.2	20	1	US-08-269-766-21	Sequence 21, Appl
c1301	14.4	0.2	20	1	US-09-198-452A-3452	Sequence 3452, Ap	1374	14.2	0.2	20	1	US-08-479-487-76	Sequence 76, Appl
c1302	14.4	0.2	20	1	US-09-198-452A-3870	Sequence 3870, Ap	c1375	14.2	0.2	20	1	US-07-951-715A-57	Sequence 57, Appl
c1303	14.4	0.2	20	1	US-09-808-358-18	Sequence 18, Appl	1376	14.2	0.2	20	1	US-08-412-431-4	Sequence 4, Appl1
c1304	14.4	0.2	20	1	US-09-808-358-44	Sequence 44, Appl	c1377	14.2	0.2	20	1	US-08-429-181-61	Sequence 61, Appl
c1305	14.4	0.2	20	1	US-09-679-299A-52	Sequence 52, Appl	1378	14.2	0.2	20	1	US-08-088-658-31	Sequence 31, Appl
1306	14.4	0.2	20	1	US-08-988-024C-16	Sequence 16, Appl	c1379	14.2	0.2	20	1	US-08-088-658-31	Sequence 31, Appl
1307	14.4	0.2	20	1	US-08-988-024C-26	Sequence 26, Appl	1380	14.2	0.2	20	1	US-08-458-393-8	Sequence 8, Appl1
1308	14.4	0.2	20	1	US-08-988-024C-27	Sequence 27, Appl	1381	14.2	0.2	20	1	US-08-623-679-4	Sequence 4, Appl1
1309	14.4	0.2	21	1	US-08-457-176-11	Sequence 11, Appl	c1382	14.2	0.2	20	1	US-08-164-386-61	Sequence 61, Appl
1310	14.4	0.2	21	1	US-08-457-175-11	Sequence 11, Appl	1383	14.2	0.2	20	1	US-08-487-141B-18	Sequence 18, Appl
c1311	14.4	0.2	21	1	US-08-336-618-27	Sequence 27, Appl	1384	14.2	0.2	20	1	US-08-487-141B-18	Sequence 18, Appl
c1312	14.4	0.2	21	1	US-08-753-147-86	Sequence 86, Appl	c1385	14.2	0.2	20	1	US-08-507-473-35	Sequence 35, Appl
1313	14.4	0.2	21	1	US-07-662-764D-12	Sequence 12, Appl	1386	14.2	0.2	20	1	US-08-417-476-39	Sequence 39, Appl
c1314	14.4	0.2	21	1	US-09-121-887-6	Sequence 6, Appl1	1387	14.2	0.2	20	1	US-08-751-282-1	Sequence 1, Appl1
c1315	14.4	0.2	21	1	US-09-241-353-6	Sequence 6, Appl1	c1388	14.2	0.2	20	1	US-08-751-282-1	Sequence 1, Appl1
c1316	14.4	0.2	21	1	US-09-245-984-6	Sequence 6, Appl1	1389	14.2	0.2	20	1	US-08-186-222-55	Sequence 55, Appl
1317	14.4	0.2	21	1	US-08-989-251-21	Sequence 21, Appl	c1390	14.2	0.2	20	1	US-08-319-556A-21	Sequence 21, Appl
c1318	14.4	0.2	21	1	US-09-241-979-6	Sequence 6, Appl1	1391	14.2	0.2	20	1	US-08-531-554-35	Sequence 35, Appl
1319	14.4	0.2	21	1	US-09-340-250-21	Sequence 21, Appl	1392	14.2	0.2	20	1	US-08-472-418-35	Sequence 35, Appl
c1320	14.4	0.2	21	1	US-08-974-549A-470	Sequence 470, App	1393	14.2	0.2	20	1	US-08-512-681-22	Sequence 22, Appl
1321	14.4	0.2	21	1	US-09-045-054-13	Sequence 13, Appl	c1394	14.2	0.2	20	1	US-08-227-108-21	Sequence 21, Appl
1322	14.4	0.2	21	1	US-09-528-108-21	Sequence 21, Appl	1395	14.2	0.2	20	1	US-08-465-485A-28	Sequence 28, Appl
1323	14.4	0.2	21	1	US-08-649-950-77	Sequence 77, Appl	c1396	14.2	0.2	20	1	US-08-628-422-13	Sequence 13, Appl
c1324	14.4	0.2	21	1	US-08-912-951-237	Sequence 237, App	1397	14.2	0.2	20	1	US-08-470-124-55	Sequence 55, Appl
c1325	14.4	0.2	21	1	US-09-659-845A-12	Sequence 12, Appl	c1398	14.2	0.2	20	1	US-08-459-448A-57	Sequence 57, Appl
1326	14.4	0.2	21	1	US-09-193-390A-12	Sequence 12, Appl	c1399	14.2	0.2	20	1	US-08-808-550-16	Sequence 16, Appl
c1327	14.4	0.2	21	1	US-09-402-181B-470	Sequence 470, App	c1400	14.2	0.2	20	1	US-08-628-145-22	Sequence 22, Appl
c1328	14.4	0.2	21	1	US-09-721-456-470	Sequence 470, App	1401	14.2	0.2	20	1	US-08-927-561-18	Sequence 18, Appl
1329	14.4	0.2	22	1	US-09-526-193A-188	Sequence 188, App	1402	14.2	0.2	20	1	US-08-927-561-19	Sequence 19, Appl
c1330	14.4	0.2	22	1	US-08-611-155B-1	Sequence 1, Appl1	c1403	14.2	0.2	20	1	US-08-902-655A-35	Sequence 35, Appl
c1331	14.4	0.2	22	1	US-08-611-155B-2	Sequence 2, Appl1	c1404	14.2	0.2	20	1	US-07-923-871C-5	Sequence 5, Appl1
c1332	14.4	0.2	22	1	US-08-611-155B-6	Sequence 6, Appl1	1405	14.2	0.2	20	1	US-08-954-391-1	Sequence 1, Appl1
c1333	14.4	0.2	22	1	US-08-231-894A-3	Sequence 3, Appl1	c1406	14.2	0.2	20	1	US-08-954-391-1	Sequence 1, Appl1
c1334	14.4	0.2	22	1	US-08-916-120A-1	Sequence 1, Appl1	1407	14.2	0.2	20	1	US-09-116-780-8	Sequence 8, Appl1
c1335	14.4	0.2	22	1	US-08-916-120A-2	Sequence 2, Appl1	c1408	14.2	0.2	20	1	US-08-756-806A-28	Sequence 28, Appl
c1336	14.4	0.2	22	1	US-08-916-120A-6	Sequence 6, Appl1	1409	14.2	0.2	20	1	US-08-476-712-2	Sequence 2, Appl1
1337	14.4	0.2	22	1	US-08-545-196B-36	Sequence 36, Appl	c1410	14.2	0.2	20	1	US-09-048-804-2	Sequence 2, Appl1
c1338	14.4	0.2	22	1	US-08-943-731-557	Sequence 557, App	c1411	14.2	0.2	20	1	US-08-665-202-127	Sequence 127, App
c1339	14.4	0.2	22	1	US-09-564-805-198	Sequence 198, App	c1412	14.2	0.2	20	1	US-08-968-542C-8	Sequence 8, Appl1
c1340	14.4	0.2	22	1	US-09-684-855-5	Sequence 5, Appl	1413	14.2	0.2	20	1	US-08-471-907A-31	Sequence 31, Appl
c1341	14.4	0.2	22	1	US-09-862-660-14	Sequence 14, Appl	c1414	14.2	0.2	20	1	US-08-471-907A-31	Sequence 31, Appl
c1342	14.4	0.2	24	1	US-09-721-154-4	Sequence 4, Appl1	c1415	14.2	0.2	20	1	US-09-092-988-21	Sequence 21, Appl
c1343	14.4	0.2	24	1	US-09-721-154-1	Sequence 1, Appl1	c1416	14.2	0.2	20	1	US-09-073-674-21	Sequence 21, Appl
c1344	14.4	0.2	24	1	US-08-487-799-17	Sequence 17, Appl	c1417	14.2	0.2	20	1	US-08-904-901-132	Sequence 132, App
c1345	14.4	0.2	26	1	US-08-747-536-17	Sequence 17, Appl	c1418	14.2	0.2	20	1	US-08-914-961-6	Sequence 6, Appl1
c1346	14.4	0.2	29	1	US-09-304-232-152	Sequence 152, App	c1419	14.2	0.2	20	1	US-08-459-592A-57	Sequence 57, Appl
c1347	14.2	0.2	15	1	US-08-882-649A-7	Sequence 7, Appl1	c1420	14.2	0.2	20	1	US-08-483-746A-13	Sequence 13, Appl

1421	14.2	0.2	20	1	US-08-483-746A-17	Sequence 17, Appl	c1494	14.2	0.2	20	1	US-09-702-246-39	Sequence 39, Appl
1422	14.2	0.2	20	1	US-08-933-774-4	Sequence 4, Appl	c1495	14.2	0.2	20	1	US-09-044-781A-14	Sequence 14, Appl
1423	14.2	0.2	20	1	US-09-080-285-28	Sequence 28, Appl	c1496	14.2	0.2	20	1	US-09-387-341-223	Sequence 223, Appl
1424	14.2	0.2	20	1	US-09-289-267-96	Sequence 96, Appl	1497	14.2	0.2	20	1	US-09-851-696-84	Sequence 84, Appl
c1425	14.2	0.2	20	1	US-08-417-089-10	Sequence 10, Appl	c1498	14.2	0.2	20	1	US-09-506-073-30	Sequence 30, Appl
1426	14.2	0.2	20	1	US-08-441-971-147	Sequence 147, Appl	1499	14.2	0.2	20	1	US-09-724-426-28	Sequence 28, Appl
c1427	14.2	0.2	20	1	US-08-459-504B-57	Sequence 57, Appl	c1500	14.2	0.2	20	1	US-08-697-626A-7	Sequence 7, Appl
1428	14.2	0.2	20	1	US-09-116-622-35	Sequence 35, Appl	c1501	14.2	0.2	20	1	US-09-597-735-29	Sequence 29, Appl
1429	14.2	0.2	20	1	US-09-166-186-68	Sequence 68, Appl	1502	14.2	0.2	20	1	US-09-657-452A-72	Sequence 72, Appl
1430	14.2	0.2	20	1	US-09-166-186-130	Sequence 130, Appl	c1503	14.2	0.2	20	1	US-09-702-327-65	Sequence 65, Appl
c1431	14.2	0.2	20	1	US-09-143-214-28	Sequence 28, Appl	c1504	14.2	0.2	20	1	US-09-444-295-29	Sequence 29, Appl
c1432	14.2	0.2	20	1	US-09-000-136-14	Sequence 14, Appl	c1505	14.2	0.2	20	1	US-09-780-175-132	Sequence 132, Appl
c1433	14.2	0.2	20	1	US-08-545-809A-72	Sequence 72, Appl	1506	14.2	0.2	20	1	US-09-907-843-39	Sequence 39, Appl
c1434	14.2	0.2	20	1	US-09-344-914-72	Sequence 72, Appl	c1507	14.2	0.2	20	1	US-09-907-843-87	Sequence 87, Appl
c1435	14.2	0.2	20	1	US-09-344-914-73	Sequence 73, Appl	1508	14.2	0.2	20	1	US-09-470-443-113	Sequence 113, Appl
c1436	14.2	0.2	20	1	US-09-249-730-132	Sequence 132, Appl	c1509	14.2	0.2	20	1	US-09-658-679A-66	Sequence 66, Appl
c1437	14.2	0.2	20	1	US-08-459-444-57	Sequence 57, Appl	1510	14.2	0.2	20	1	US-09-676-610B-60	Sequence 60, Appl
1438	14.2	0.2	20	1	US-09-418-641-12	Sequence 12, Appl	c1511	14.2	0.2	20	1	US-09-676-610B-118	Sequence 118, Appl
1439	14.2	0.2	20	1	US-09-091-899-8	Sequence 8, Appl	c1512	14.2	0.2	20	1	US-09-853-768-44	Sequence 44, Appl
c1440	14.2	0.2	20	1	US-08-695-651-10	Sequence 10, Appl	1513	14.2	0.2	20	1	US-09-328-174A-83	Sequence 83, Appl
c1441	14.2	0.2	20	1	US-08-765-340-35	Sequence 35, Appl	1514	14.2	0.2	20	1	US-09-328-174A-84	Sequence 84, Appl
1442	14.2	0.2	20	1	US-08-765-340-90	Sequence 90, Appl	1515	14.2	0.2	20	1	US-09-791-211-66	Sequence 66, Appl
c1443	14.2	0.2	20	1	US-09-135-021-27	Sequence 27, Appl	c1516	14.2	0.2	20	1	US-09-441-340-22	Sequence 22, Appl
c1444	14.2	0.2	20	1	US-09-106-216-21	Sequence 21, Appl	c1517	14.2	0.2	20	1	US-09-597-732-29	Sequence 29, Appl
c1445	14.2	0.2	20	1	US-09-429-034-21	Sequence 21, Appl	c1518	14.2	0.2	20	1	US-09-746-694-42	Sequence 42, Appl
c1446	14.2	0.2	20	1	US-09-433-639-64	Sequence 64, Appl	c1519	14.2	0.2	20	1	US-09-517-467B-58	Sequence 58, Appl
1447	14.2	0.2	20	1	US-09-428-219-15	Sequence 15, Appl	c1520	14.2	0.2	20	1	US-09-091-952A-58	Sequence 58, Appl
c1448	14.2	0.2	20	1	US-09-490-692-167	Sequence 167, Appl	c1521	14.2	0.2	20	1	US-09-360-416-43	Sequence 43, Appl
1449	14.2	0.2	20	1	US-09-488-671-98	Sequence 98, Appl	c1522	14.2	0.2	20	1	US-09-657-346A-151	Sequence 151, Appl
c1450	14.2	0.2	20	1	US-09-517-584A-63	Sequence 63, Appl	1523	14.2	0.2	20	1	US-09-780-049-25	Sequence 25, Appl
c1451	14.2	0.2	20	1	US-08-766-528-68	Sequence 68, Appl	1524	14.2	0.2	20	1	US-09-305-856B-73	Sequence 73, Appl
1452	14.2	0.2	20	1	US-08-221-653-147	Sequence 147, Appl	c1525	14.2	0.2	20	1	US-09-725-265-34	Sequence 34, Appl
c1453	14.2	0.2	20	1	US-09-219-277-35	Sequence 35, Appl	c1526	14.2	0.2	20	1	US-09-658-688A-21	Sequence 21, Appl
1454	14.2	0.2	20	1	US-09-253-025-6	Sequence 6, Appl	c1527	14.2	0.2	20	1	US-09-657-346A-14	Sequence 14, Appl
1455	14.2	0.2	20	1	US-08-442-144A-147	Sequence 147, Appl	c1528	14.2	0.2	20	1	US-09-668-113A-44	Sequence 44, Appl
c1456	14.2	0.2	20	1	US-09-446-504-31	Sequence 31, Appl	c1529	14.2	0.2	20	1	US-09-315-574-127	Sequence 127, Appl
c1457	14.2	0.2	20	1	US-08-930-285-10	Sequence 10, Appl	c1530	14.2	0.2	20	1	US-08-754-477A-92	Sequence 92, Appl
c1458	14.2	0.2	20	1	US-08-930-285-24	Sequence 24, Appl	1531	14.2	0.2	20	1	US-09-422-978-4737	Sequence 4737, Appl
c1459	14.2	0.2	20	1	US-09-476-256-12	Sequence 12, Appl	1532	14.2	0.2	20	1	US-09-422-978-8838	Sequence 8838, Appl
c1460	14.2	0.2	20	1	US-09-476-256-17	Sequence 17, Appl	1533	14.2	0.2	20	1	US-09-422-978-10868	Sequence 10868, A
c1461	14.2	0.2	20	1	US-09-599-661-35	Sequence 35, Appl	c1534	14.2	0.2	20	1	US-08-857-336-11	Sequence 11, Appl
1462	14.2	0.2	20	1	US-09-313-932-68	Sequence 68, Appl	1535	14.2	0.2	20	1	US-09-198-452A-1307	Sequence 1307, Appl
1463	14.2	0.2	20	1	US-09-313-932-130	Sequence 130, Appl	1536	14.2	0.2	20	1	US-09-198-452A-1575	Sequence 1575, Appl
c1464	14.2	0.2	20	1	US-09-313-932-297	Sequence 297, Appl	1537	14.2	0.2	20	1	US-09-198-452A-1693	Sequence 1693, Appl
1465	14.2	0.2	20	1	US-08-427-569-55	Sequence 55, Appl	c1538	14.2	0.2	20	1	US-09-198-452A-1958	Sequence 1958, Appl
c1466	14.2	0.2	20	1	US-09-560-594-59	Sequence 59, Appl	c1539	14.2	0.2	20	1	US-09-198-452A-2176	Sequence 2176, Appl
c1467	14.2	0.2	20	1	US-09-021-701-669	Sequence 669, Appl	c1540	14.2	0.2	20	1	US-09-198-452A-2534	Sequence 2534, Appl
c1468	14.2	0.2	20	1	US-09-021-701-670	Sequence 670, Appl	1541	14.2	0.2	20	1	US-09-198-452A-2989	Sequence 2989, Appl
1469	14.2	0.2	20	1	US-09-021-701-737	Sequence 737, Appl	1542	14.2	0.2	20	1	US-09-198-452A-3434	Sequence 3434, Appl
1470	14.2	0.2	20	1	US-09-021-701-773	Sequence 773, Appl	1543	14.2	0.2	20	1	US-09-198-452A-4619	Sequence 4619, Appl
1471	14.2	0.2	20	1	US-09-021-701-774	Sequence 774, Appl	1544	14.2	0.2	20	1	US-09-198-452A-4967	Sequence 4967, Appl
1472	14.2	0.2	20	1	US-09-181-030-4	Sequence 4, Appl	1545	14.2	0.2	20	1	US-09-198-452A-5175	Sequence 5175, Appl
c1473	14.2	0.2	20	1	US-09-489-869-15	Sequence 15, Appl	1546	14.2	0.2	20	1	US-09-198-452A-6067	Sequence 6067, Appl
c1474	14.2	0.2	20	1	US-08-695-421-10	Sequence 10, Appl	c1547	14.2	0.2	20	1	US-09-198-452A-6287	Sequence 6287, Appl
1475	14.2	0.2	20	1	US-09-593-711A-54	Sequence 54, Appl	c1548	14.2	0.2	20	1	US-09-198-452A-6290	Sequence 6290, Appl
c1476	14.2	0.2	20	1	US-09-593-711A-228	Sequence 228, Appl	c1549	14.2	0.2	20	1	US-09-198-452A-6683	Sequence 6683, Appl
c1477	14.2	0.2	20	1	US-09-135-020-29	Sequence 29, Appl	c1550	14.2	0.2	20	1	US-09-597-731-29	Sequence 29, Appl
1478	14.2	0.2	20	1	US-09-230-804-6	Sequence 6, Appl	1551	14.2	0.2	20	1	US-09-909-595-83	Sequence 83, Appl
c1479	14.2	0.2	20	1	US-09-135-010A-29	Sequence 29, Appl	c1552	14.2	0.2	20	1	US-09-249-447-132	Sequence 132, Appl
1480	14.2	0.2	20	1	US-08-441-970-147	Sequence 147, Appl	c1553	14.2	0.2	20	1	US-10-072-094-105	Sequence 105, Appl
1481	14.2	0.2	20	1	US-08-169-715-56	Sequence 56, Appl	c1554	14.2	0.2	20	1	US-09-780-045-37	Sequence 37, Appl
1482	14.2	0.2	20	1	US-09-411-291-2	Sequence 2, Appl	1555	14.2	0.2	20	1	US-09-780-045-93	Sequence 93, Appl
c1483	14.2	0.2	20	1	US-09-721-822A-90	Sequence 90, Appl	c1556	14.2	0.2	20	1	US-09-112-580-41	Sequence 41, Appl
1484	14.2	0.2	20	1	US-09-534-242-4	Sequence 4, Appl	c1557	14.2	0.2	20	1	US-09-554-678A-8	Sequence 8, Appl
1485	14.2	0.2	20	1	US-09-454-854-4	Sequence 4, Appl	1558	14.2	0.2	20	1	US-09-554-726A-29	Sequence 29, Appl
c1486	14.2	0.2	20	1	US-09-547-422-57	Sequence 57, Appl	1559	14.2	0.2	20	1	US-09-734-188-6	Sequence 6, Appl
c1487	14.2	0.2	20	1	US-09-444-871-39	Sequence 39, Appl	c1560	14.2	0.2	20	1	US-09-495-714C-77	Sequence 77, Appl
c1488	14.2	0.2	20	1	US-09-712-266-31	Sequence 31, Appl	c1561	14.2	0.2	20	1	PCT-US91-0157A-5	Sequence 5, Appl
c1489	14.2	0.2	20	1	US-09-651-011A-14	Sequence 14, Appl	c1562	14.2	0.2	20	1	PCT-US93-0774A-14	Sequence 14, Appl
1490	14.2	0.2	20	1	US-09-388-349-10	Sequence 10, Appl	c1563	14.2	0.2	20	1	PCT-US95-07111A-18	Sequence 18, Appl
1491	14.2	0.2	20	1	US-09-662-250A-68	Sequence 68, Appl	1564	14.2	0.2	20	1	PCT-US96-09388-18	Sequence 18, Appl
1492	14.2	0.2	20	1	US-09-164-671-4	Sequence 4, Appl	1565	14.2	0.2	20	1	PCT-US96-09388-19	Sequence 19, Appl
1493	14.2	0.2	20	1	US-09-177-437-8	Sequence 8, Appl	1566	14.2	0.2	21	1	US-08-424-663-5	Sequence 5, Appl

1567	14.2	0.2	21	1	US-08-872-446-5	Sequence 5, Appl1	1640	14.2	0.2	21	1	US-09-422-978-10757	Sequence 10757, A
1568	14.2	0.2	21	1	US-09-280-270A-5	Sequence 5, Appl1	1641	14.2	0.2	21	1	US-09-422-978-11155	Sequence 11155, A
1569	14.2	0.2	21	1	US-07-873-915A-1	Sequence 1, Appl1	1642	14.2	0.2	21	1	US-09-422-978-11515	Sequence 11515, A
1570	14.2	0.2	21	1	US-07-932-379A-19	Sequence 19, Appl1	1643	14.2	0.2	21	1	US-09-422-978-11524	Sequence 11524, A
1571	14.2	0.2	21	1	US-08-042-747A-2	Sequence 2, Appl1	1644	14.2	0.2	21	1	US-09-404-641-29	Sequence 29, Appl1
1572	14.2	0.2	21	1	US-08-063-167A-36	Sequence 36, Appl1	1645	14.2	0.2	21	1	US-09-175-684A-16	Sequence 16, Appl1
1573	14.2	0.2	21	1	US-08-379-295-19	Sequence 19, Appl1	1646	14.2	0.2	21	1	US-09-923-246-11	Sequence 11, Appl1
1574	14.2	0.2	21	1	US-08-257-964-1	Sequence 1, Appl1	1647	14.2	0.2	21	1	US-09-923-246-51	Sequence 51, Appl1
1575	14.2	0.2	21	1	US-08-379-296-19	Sequence 19, Appl1	1648	14.2	0.2	21	1	US-09-402-181B-514	Sequence 514, App
1576	14.2	0.2	21	1	US-08-136-118-3	Sequence 3, Appl1	1649	14.2	0.2	21	1	US-09-721-456-514	Sequence 514, App
1577	14.2	0.2	21	1	US-08-007-997A-36	Sequence 36, Appl1	1650	14.2	0.2	21	1	US-09-486-147-19	Sequence 19, Appl1
1578	14.2	0.2	21	1	US-08-076-090-3	Sequence 3, Appl1	1651	14.2	0.2	21	1	US-09-723-909-34	Sequence 34, Appl1
1579	14.2	0.2	21	1	US-08-076-090-4	Sequence 4, Appl1	1652	14.2	0.2	21	1	US-09-908-410-9	Sequence 9, Appl1
1580	14.2	0.2	21	1	US-08-445-746-6	Sequence 6, Appl1	1653	14.2	0.2	21	1	US-09-726-774-54	Sequence 54, Appl1
1581	14.2	0.2	21	1	US-08-438-639-1	Sequence 1, Appl1	1654	14.2	0.2	21	1	US-09-726-774-73	Sequence 73, Appl1
1582	14.2	0.2	21	1	US-08-446-600A-6	Sequence 6, Appl1	1655	14.2	0.2	21	1	US-09-077-773-19	Sequence 19, Appl1
1583	14.2	0.2	21	1	US-07-813-338A-1	Sequence 1, Appl1	1656	14.2	0.2	21	1	US-09-870-958-27	Sequence 27, Appl1
1584	14.2	0.2	21	1	US-08-211-430-8	Sequence 8, Appl1	1657	14.2	0.2	21	1	US-10-065-135A-60	Sequence 60, Appl1
1585	14.2	0.2	21	1	US-08-753-147-24	Sequence 24, Appl1	1658	14.2	0.2	21	1	US-10-295-723-11	Sequence 11, Appl1
1586	14.2	0.2	21	1	US-08-592-936B-19	Sequence 19, Appl1	1659	14.2	0.2	21	1	US-10-295-723-51	Sequence 51, Appl1
1587	14.2	0.2	21	1	US-08-110-691A-30	Sequence 30, Appl1	1660	14.2	0.2	21	1	PCT-US93-08101-36	Sequence 36, Appl1
1588	14.2	0.2	21	1	US-08-465-590-34	Sequence 34, Appl1	1661	14.2	0.2	21	1	PCT-US94-06651-3	Sequence 3, Appl1
1589	14.2	0.2	21	1	US-08-472-659-27	Sequence 27, Appl1	1662	14.2	0.2	21	1	PCT-US94-06651-4	Sequence 4, Appl1
1590	14.2	0.2	21	1	US-08-538-816A-6	Sequence 6, Appl1	1663	14.2	0.2	21	1	PCT-US96-09430-8	Sequence 8, Appl1
1591	14.2	0.2	21	1	US-08-639-080-31	Sequence 31, Appl1	1664	14.2	0.2	21	1	PCT-US96-09430-9	Sequence 9, Appl1
1592	14.2	0.2	21	1	US-08-440-740A-35	Sequence 35, Appl1	1665	14.2	0.2	21	1	PCT-US96-09430-11	Sequence 11, Appl1
1593	14.2	0.2	21	1	US-08-173-489C-115	Sequence 115, App	1666	14.2	0.2	26	1	US-09-167-511-10	Sequence 10, Appl1
1594	14.2	0.2	21	1	US-08-173-489C-117	Sequence 117, App	1667	14.2	0.2	26	1	US-09-161-932A-43	Sequence 43, Appl1
1595	14.2	0.2	21	1	US-08-173-489C-118	Sequence 118, App	1668	14.2	0.2	28	1	US-08-858-767-14	Sequence 14, Appl1
1596	14.2	0.2	21	1	US-08-474-661-27	Sequence 27, Appl1	1669	14.2	0.2	30	1	US-08-863-028-14	Sequence 14, Appl1
1597	14.2	0.2	21	1	US-08-740-215B-3	Sequence 3, Appl1	1670	14.2	0.2	30	1	US-08-455-627-12	Sequence 12, Appl1
1598	14.2	0.2	21	1	US-09-076-651-6	Sequence 6, Appl1	1671	14.2	0.2	30	1	US-08-689-856-12	Sequence 12, Appl1
1599	14.2	0.2	21	1	US-08-344-155C-36	Sequence 36, Appl1	1672	14.2	0.2	30	1	US-08-787-321-12	Sequence 12, Appl1
1600	14.2	0.2	21	1	US-09-111-573-19	Sequence 19, Appl1	1673	14.2	0.2	30	1	US-09-725-265-4	Sequence 4, Appl1
1601	14.2	0.2	21	1	US-09-213-767-3	Sequence 3, Appl1	1674	14.2	0.2	30	1	US-08-173-489C-75	Sequence 75, Appl1
1602	14.2	0.2	21	1	US-08-611-977-27	Sequence 27, Appl1	1675	14.2	0.2	14	1	US-08-173-489C-76	Sequence 76, Appl1
1603	14.2	0.2	21	1	US-08-867-941-48	Sequence 48, Appl1	1676	14.2	0.2	14	1	US-08-832-021-16	Sequence 16, Appl1
1604	14.2	0.2	21	1	US-08-487-799-75	Sequence 75, Appl1	1677	14.2	0.2	14	1	US-08-724-466B-14	Sequence 14, Appl1
1605	14.2	0.2	21	1	US-08-804-439A-31	Sequence 31, Appl1	1678	14.2	0.2	14	1	US-08-787-321-6	Sequence 6, Appl1
1606	14.2	0.2	21	1	US-09-008-722-6	Sequence 6, Appl1	1679	14.2	0.2	14	1	US-09-019-095A-26	Sequence 26, Appl1
1607	14.2	0.2	21	1	US-08-982-845B-36	Sequence 36, Appl1	1680	14.2	0.2	14	1	US-08-882-164D-14	Sequence 14, Appl1
1608	14.2	0.2	21	1	US-08-720-229-31	Sequence 31, Appl1	1681	14.2	0.2	14	1	US-09-462-565B-1	Sequence 1, Appl1
1609	14.2	0.2	21	1	US-08-081-180-28	Sequence 28, Appl1	1682	14.2	0.2	14	1	US-09-619-103-20	Sequence 20, Appl1
1610	14.2	0.2	21	1	US-09-040-786-28	Sequence 28, Appl1	1683	14.2	0.2	14	1	5453496-4	Patent No. 5453496
1611	14.2	0.2	21	1	US-08-746-111-3	Sequence 3, Appl1	1684	14.2	0.2	14	1	5453496-5	Patent No. 5453496
1612	14.2	0.2	21	1	US-08-991-525B-36	Sequence 36, Appl1	1685	14.2	0.2	15	1	US-08-452-196A-3	Sequence 3, Appl1
1613	14.2	0.2	21	1	US-09-085-759-36	Sequence 36, Appl1	1686	14.2	0.2	15	1	US-08-452-196A-4	Sequence 4, Appl1
1614	14.2	0.2	21	1	US-09-344-914-2	Sequence 2, Appl1	1687	14.2	0.2	15	1	US-08-358-995-25	Sequence 25, Appl1
1615	14.2	0.2	21	1	US-08-974-549A-514	Sequence 514, App	1688	14.2	0.2	15	1	US-08-292-620A-360	Sequence 360, App
1616	14.2	0.2	21	1	US-09-128-496-36	Sequence 36, Appl1	1689	14.2	0.2	15	1	US-08-292-620A-363	Sequence 363, App
1617	14.2	0.2	21	1	US-09-235-614-31	Sequence 31, Appl1	1690	14.2	0.2	15	1	US-08-832-021-61	Sequence 61, App
1618	14.2	0.2	21	1	US-09-074-658-48	Sequence 48, Appl1	1691	14.2	0.2	15	1	US-08-832-021-63	Sequence 63, Appl1
1619	14.2	0.2	21	1	US-09-045-054-34	Sequence 34, Appl1	1692	14.2	0.2	15	1	US-08-832-021-63	Sequence 63, Appl1
1620	14.2	0.2	21	1	US-08-711-417C-34	Sequence 34, Appl1	1693	14.2	0.2	15	1	US-09-071-845-360	Sequence 360, App
1621	14.2	0.2	21	1	US-08-943-731-490	Sequence 490, App	1694	14.2	0.2	15	1	US-09-071-845-363	Sequence 363, App
1622	14.2	0.2	21	1	US-09-268-140-15	Sequence 15, Appl1	1695	14.2	0.2	15	1	US-09-071-845-365	Sequence 365, App
1623	14.2	0.2	21	1	US-09-068-319-3	Sequence 3, Appl1	1696	14.2	0.2	15	1	US-09-071-845-556	Sequence 556, App
1624	14.2	0.2	21	1	US-09-109-663-49	Sequence 49, Appl1	1697	14.2	0.2	15	1	US-09-163-485-13	Sequence 13, Appl1
1625	14.2	0.2	21	1	US-09-009-490A-36	Sequence 36, Appl1	1698	14.2	0.2	15	1	US-09-475-947A-158	Sequence 158, App
1626	14.2	0.2	21	1	US-09-522-217-11	Sequence 11, Appl1	1699	14.2	0.2	15	1	US-09-475-947A-304	Sequence 304, App
1627	14.2	0.2	21	1	US-09-522-217-51	Sequence 51, Appl1	1700	14.2	0.2	17	1	PCT-US91-03680-16	Sequence 16, Appl1
1628	14.2	0.2	21	1	US-09-208-394-6	Sequence 6, Appl1	1701	14.2	0.2	17	1	US-08-584-040-2546	Sequence 2546, App
1629	14.2	0.2	21	1	US-09-177-650-23	Sequence 23, Appl1	1702	14.2	0.2	17	1	US-08-584-040-2553	Sequence 2553, App
1630	14.2	0.2	21	1	US-09-328-174A-74	Sequence 74, Appl1	1703	14.2	0.2	17	1	US-09-371-772B-1070	Sequence 1070, App
1631	14.2	0.2	21	1	US-08-912-951-281	Sequence 281, Appl1	1704	14.2	0.2	17	1	US-09-371-772B-1077	Sequence 1077, App
1632	14.2	0.2	21	1	US-09-506-286B-60	Sequence 60, Appl1	1705	14.2	0.2	17	1	US-09-554-726A-22	Sequence 22, Appl1
1633	14.2	0.2	21	1	US-09-559-773A-4	Sequence 4, Appl1	1706	14.2	0.2	17	1	US-09-866-108A-1536	Sequence 1536, App
1634	14.2	0.2	21	1	US-09-636-382A-10	Sequence 10, Appl1	1707	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, App
1635	14.2	0.2	21	1	US-09-422-978-6188	Sequence 6188, App	1708	14.2	0.2	17	1	US-09-866-108A-7979	Sequence 7979, App
1636	14.2	0.2	21	1	US-09-422-978-8873	Sequence 8873, App	1709	14.2	0.2	17	1	US-09-866-108A-7980	Sequence 7980, App
1637	14.2	0.2	21	1	US-09-422-978-8873	Sequence 8873, App	1710	14.2	0.2	18	1	US-08-066-325-52	Sequence 52, Appl1
1638	14.2	0.2	21	1	US-09-422-978-10601	Sequence 10601, A	1711	14.2	0.2	18	1	US-07-938-906-8	Sequence 8, Appl1
1639	14.2	0.2	21	1	US-09-422-978-10694	Sequence 10694, A	1712	14.2	0.2	18	1		

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c1714	14	0.2	18	1	US-08-633-358-8	Sequence 8, Appli	1787	14	0.2	22	1	US-08-458-050-19	Sequence 19, Appl
c1715	14	0.2	18	1	US-09-225-911-31	Sequence 31, Appl	1788	14	0.2	22	1	US-08-847-844A-94	Sequence 19, Appl
c1716	14	0.2	18	1	US-09-289-376-45	Sequence 45, Appl	1789	14	0.2	22	1	US-08-950-196-19	Sequence 19, Appl
c1717	14	0.2	18	1	US-08-559-205-28	Sequence 28, Appl	1790	14	0.2	22	1	US-09-720-201A-25	Sequence 25, Appl
1718	14	0.2	18	1	US-09-630-706-41	Sequence 41, Appl	c1791	14	0.2	22	1	US-08-123-449A-1	Sequence 1, Appli
1719	14	0.2	18	1	US-09-423-978-4090	Sequence 4090, Ap	c1792	14	0.2	22	1	US-08-123-449A-2	Sequence 2, Appli
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1721	14	0.2	18	1	US-09-423-978-8891	Sequence 8891, Ap	c1794	14	0.2	22	1	US-08-458-050-2	Sequence 2, Appli
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c1724	14	0.2	19	1	US-08-423-383-24	Sequence 24, Appli	1797	14	0.2	22	1	US-09-750-401-17	Sequence 17, Appl
c1725	14	0.2	19	1	US-08-423-383-51	Sequence 51, Appl	1798	14	0.2	22	1	US-09-750-401-19	Sequence 19, Appl
c1726	14	0.2	19	1	US-08-620-457A-62	Sequence 62, Appl	c1799	14	0.2	22	1	US-08-457-273B-31	Sequence 31, Appl
c1727	14	0.2	19	1	US-08-348-572-63	Sequence 63, Appl	1800	14	0.2	23	1	US-07-869-933-7	Sequence 7, Appli
c1728	14	0.2	19	1	US-08-437-353A-24	Sequence 24, Appl	1801	14	0.2	23	1	US-09-103-663-7	Sequence 7, Appli
c1729	14	0.2	19	1	US-08-437-353A-51	Sequence 51, Appl	1802	14	0.2	24	1	US-08-014-943B-25	Sequence 25, Appl
c1730	14	0.2	19	1	US-08-468-037A-33	Sequence 33, Appl	1803	14	0.2	24	1	US-08-486-421-50	Sequence 50, Appl
c1731	14	0.2	19	1	US-08-471-973A-33	Sequence 33, Appl	1804	14	0.2	24	1	US-08-470-911-50	Sequence 50, Appl
c1732	14	0.2	19	1	US-08-466-880-28	Sequence 28, Appl	1805	14	0.2	24	1	US-08-735-381-1	Sequence 1, Appli
c1733	14	0.2	19	1	US-09-035-357-33	Sequence 33, Appl	1806	14	0.2	24	1	US-08-486-809-50	Sequence 50, Appl
c1734	14	0.2	19	1	US-09-199-859-3	Sequence 3, Appli	1807	14	0.2	24	1	US-09-183-619-7	Sequence 7, Appli
c1735	14	0.2	19	1	US-09-041-090B-63	Sequence 63, Appli	1808	14	0.2	24	1	US-09-201-674-1	Sequence 1, Appli
c1736	14	0.2	19	1	US-09-016-520-4	Sequence 4, Appli	1809	14	0.2	24	1	US-09-536-936-11	Sequence 11, Appl
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c1738	14	0.2	19	1	US-09-135-021-65	Sequence 65, Appl	1811	14	0.2	24	1	US-09-333-237-4	Sequence 4, Appli
c1739	14	0.2	19	1	US-09-130-973-4	Sequence 4, Appli	1812	14	0.2	24	1	US-09-732-067-1	Sequence 1, Appli
c1740	14	0.2	19	1	US-09-477-902-4	Sequence 4, Appli	1813	14	0.2	24	1	US-10-043-415-4	Sequence 4, Appli
c1741	14	0.2	19	1	US-09-338-907-568	Sequence 568, App	1814	14	0.2	24	1	US-09-854-317-1	Sequence 1, Appli
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c1744	14	0.2	19	1	US-09-135-010A-67	Sequence 67, Appl	1817	14	0.2	24	1	US-08-924-695A-22	Sequence 22, Appl
c1745	14	0.2	19	1	US-09-444-871-67	Sequence 67, Appl	c1818	14	0.2	25	1	US-08-341-148-2	Sequence 2, Appli
c1746	14	0.2	19	1	US-09-453-514A-12	Sequence 12, Appl	c1819	14	0.2	25	1	US-08-460-130-2	Sequence 2, Appli
c1747	14	0.2	19	1	US-09-218-207-568	Sequence 568, App	c1820	14	0.2	25	1	US-08-969-913-1	Sequence 1, Appli
c1748	14	0.2	19	1	US-09-218-207-573	Sequence 573, App	c1821	14	0.2	25	1	US-09-183-619-5	Sequence 5, Appli
c1749	14	0.2	19	1	US-09-135-202-33	Sequence 33, Appl	c1822	14	0.2	25	1	US-09-282-734-23	Sequence 23, Appl
c1750	14	0.2	19	1	US-09-597-735-67	Sequence 67, Appl	c1823	14	0.2	25	1	PCT-US94-14096-2	Sequence 2, Appli
c1751	14	0.2	19	1	US-09-444-295-67	Sequence 67, Appl	c1824	14	0.2	26	1	US-08-621-814A-3	Sequence 3, Appli
c1752	14	0.2	19	1	US-09-597-732-67	Sequence 67, Appl	1825	14	0.2	26	1	US-08-910-632-5	Sequence 5, Appli
c1753	14	0.2	19	1	US-08-802-331-29	Sequence 29, Appl	1826	14	0.2	26	1	US-08-805-531A-5	Sequence 5, Appli
c1754	14	0.2	19	1	US-09-389-283-33	Sequence 33, Appl	1827	14	0.2	26	1	US-09-569-444-5	Sequence 5, Appli
1755	14	0.2	19	1	US-09-423-978-9216	Sequence 9216, Ap	c1828	14	0.2	32	1	US-08-784-208-3	Sequence 3, Appli
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c1757	14	0.2	19	1	US-08-442-001C-62	Sequence 62, Appl	1830	13.8	0.2	17	1	US-08-373-124A-1054	Sequence 1054, Ap
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c1759	14	0.2	19	1	US-09-856-747-3	Sequence 59, Appl	c1832	13.8	0.2	17	1	US-08-373-124A-2147	Sequence 2147, Ap
1760	14	0.2	20	1	US-09-560-594-59	Sequence 59, Appl	c1833	13.8	0.2	17	1	US-08-327-825A-6	Sequence 6, Appli
1761	14	0.2	20	1	US-07-984-044A-25	Sequence 25, Appl	c1834	13.8	0.2	17	1	US-08-758-306-453	Sequence 453, App
1762	14	0.2	20	1	US-08-088-658-53	Sequence 33, Appl	1835	13.8	0.2	17	1	US-08-758-306-661	Sequence 661, App
1763	14	0.2	20	1	US-08-458-393-25	Sequence 15, Appl	c1836	13.8	0.2	17	1	US-08-435-628-970	Sequence 970, App
1764	14	0.2	20	1	US-08-117-952-15	Sequence 15, Appl	1837	13.8	0.2	17	1	US-08-435-628-1054	Sequence 1054, App
1765	14	0.2	20	1	US-08-471-907A-33	Sequence 33, Appl	1838	13.8	0.2	17	1	US-08-435-628-1967	Sequence 1967, Ap
1766	14	0.2	20	1	US-09-280-805-79	Sequence 79, Appl	1839	13.8	0.2	17	1	US-08-435-628-2147	Sequence 2147, Ap
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c1768	14	0.2	20	1	US-09-517-584A-81	Sequence 81, Appl	1841	13.8	0.2	17	1	US-08-438-864-20	Sequence 20, Appl
1769	14	0.2	20	1	US-09-844-634-64	Sequence 64, Appl	c1842	13.8	0.2	17	1	US-08-531-137B-6	Sequence 6, Appli
c1770	14	0.2	20	1	US-09-470-443-64	Sequence 64, Appl	1843	13.8	0.2	17	1	US-08-985-162-434	Sequence 434, App
c1771	14	0.2	20	1	US-09-851-062-4	Sequence 4, Appli	1844	13.8	0.2	17	1	US-08-988-706-24	Sequence 24, Appl
c1772	14	0.2	20	1	US-08-275-951-46	Sequence 46, Appl	1845	13.8	0.2	17	1	US-08-913-833-56	Sequence 56, Appl
1773	14	0.2	20	1	US-09-422-978-6254	Sequence 6254, Ap	1846	13.8	0.2	17	1	US-08-628-447-20	Sequence 20, Appl
1774	14	0.2	20	1	US-09-422-978-7396	Sequence 7396, Ap	1847	13.8	0.2	17	1	US-08-402-253-20	Sequence 20, Appl
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c1776	14	0.2	20	1	US-09-198-452A-6060	Sequence 6060, Ap	1849	13.8	0.2	17	1	US-09-021-701-128	Sequence 128, App
1777	14	0.2	20	1	US-09-860-047-5	Sequence 70, Appl	1850	13.8	0.2	17	1	US-09-021-701-129	Sequence 129, App
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1779	14	0.2	21	1	US-08-403-888A-146	Sequence 146, App	1852	13.8	0.2	17	1	US-09-580-794C-36	Sequence 56, Appl
c1780	14	0.2	21	1	US-08-711-417C-167	Sequence 167, App	1853	13.8	0.2	17	1	US-08-584-040-2073	Sequence 2073, Ap
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1783	14	0.2	21	1	US-09-083-852A-9	Sequence 9, Appli	c1856	13.8	0.2	17	1	US-08-584-040-2172	Sequence 2172, Ap
c1784	14	0.2	21	1	US-09-723-909-167	Sequence 167, App	1857	13.8	0.2	17	1	US-08-584-040-3895	Sequence 3895, Ap
1785	14	0.2	21	1	US-09-927-842-30	Sequence 30, Appl	c1858	13.8	0.2	17	1	US-08-584-040-3895	Sequence 3895, Ap

1859	13.8	0.2	17	1	US-08-584-040-4028	Sequence 4028, Ap	c1932	13.8	0.2	18	1	US-08-483-522-6	Sequence 6, Appl1
c1860	13.8	0.2	17	1	US-08-584-040-5492	Sequence 5492, Ap	c1933	13.8	0.2	18	1	US-08-126-593A-9	Sequence 9, Appl1
1861	13.8	0.2	17	1	US-08-584-040-5832	Sequence 5832, Ap	c1934	13.8	0.2	18	1	US-08-411-796-263	Sequence 263, App
1862	13.8	0.2	17	1	US-08-584-040-7818	Sequence 7818, Ap	c1935	13.8	0.2	18	1	US-08-363-240A-1122	Sequence 1122, Ap
1863	13.8	0.2	17	1	US-08-584-040-7819	Sequence 7819, Ap	c1936	13.8	0.2	18	1	US-08-488-470A-15	Sequence 15, Appl1
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1866	13.8	0.2	17	1	US-08-584-040-7823	Sequence 7823, Ap	c1939	13.8	0.2	18	1	US-07-946-239-6	Sequence 6, Appl1
1867	13.8	0.2	17	1	US-08-584-040-8030	Sequence 8030, Ap	c1940	13.8	0.2	18	1	US-08-484-505A-15	Sequence 15, Appl1
c1868	13.8	0.2	17	1	US-08-679-645-61	Sequence 61, Appl1	c1941	13.8	0.2	18	1	US-08-367-066-11	Sequence 11, Appl1
1869	13.8	0.2	17	1	US-09-531-000-6	Sequence 61, Appl1	c1942	13.8	0.2	18	1	US-08-384-324-4	Sequence 4, Appl1
1870	13.8	0.2	17	1	US-09-474-432B-558	Sequence 558, App	c1943	13.8	0.2	18	1	US-08-585-684B-2587	Sequence 2587, Ap
1871	13.8	0.2	17	1	US-09-474-432B-657	Sequence 657, App	c1944	13.8	0.2	18	1	US-08-585-684B-2635	Sequence 2635, App
1872	13.8	0.2	17	1	US-09-474-432B-667	Sequence 667, App	c1945	13.8	0.2	18	1	US-08-585-684B-2687	Sequence 2687, Ap
c1873	13.8	0.2	17	1	US-09-371-772B-618	Sequence 618, App	c1946	13.8	0.2	18	1	US-08-460-751-15	Sequence 15, Appl1
c1874	13.8	0.2	17	1	US-09-371-772B-647	Sequence 647, App	c1947	13.8	0.2	18	1	US-08-951-664-14	Sequence 14, Appl1
c1875	13.8	0.2	17	1	US-09-371-772B-738	Sequence 738, App	c1948	13.8	0.2	18	1	US-08-867-941-37	Sequence 37, Appl1
c1876	13.8	0.2	17	1	US-09-371-772B-1662	Sequence 1662, Ap	c1949	13.8	0.2	18	1	US-09-205-860-10	Sequence 10, Appl1
c1877	13.8	0.2	17	1	US-09-371-772B-1795	Sequence 1795, Ap	c1950	13.8	0.2	18	1	US-08-857-946-8	Sequence 8, Appl1
c1878	13.8	0.2	17	1	US-09-371-772B-2383	Sequence 2383, Ap	c1951	13.8	0.2	18	1	US-08-857-946-14	Sequence 14, Appl1
c1879	13.8	0.2	17	1	US-09-371-772B-2692	Sequence 2692, Ap	c1952	13.8	0.2	18	1	US-09-256-496-64	Sequence 64, Appl1
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1881	13.8	0.2	17	1	US-09-371-772B-3602	Sequence 3602, Ap	c1954	13.8	0.2	18	1	US-09-156-253-8	Sequence 8, Appl1
1882	13.8	0.2	17	1	US-09-371-772B-3603	Sequence 3603, Ap	c1955	13.8	0.2	18	1	US-09-138-024-5	Sequence 5, Appl1
1883	13.8	0.2	17	1	US-09-371-772B-3604	Sequence 3604, Ap	c1956	13.8	0.2	18	1	US-09-205-921-40	Sequence 40, Appl1
1884	13.8	0.2	17	1	US-09-371-772B-3605	Sequence 3605, Ap	c1957	13.8	0.2	18	1	US-08-970-740-8	Sequence 8, Appl1
1885	13.8	0.2	17	1	US-09-371-772B-3607	Sequence 3607, Ap	c1958	13.8	0.2	18	1	US-08-471-039-263	Sequence 263, App
1886	13.8	0.2	17	1	US-09-371-772B-3813	Sequence 3813, Ap	c1959	13.8	0.2	18	1	US-09-358-381-32	Sequence 32, Appl1
c1887	13.8	0.2	17	1	US-09-371-772B-4950	Sequence 4950, Ap	c1960	13.8	0.2	18	1	US-09-358-381-32	Sequence 32, Appl1
c1888	13.8	0.2	17	1	US-09-371-772B-5350	Sequence 5350, Ap	c1961	13.8	0.2	18	1	US-09-339-964-11	Sequence 11, Appl1
c1889	13.8	0.2	17	1	US-09-371-772B-5639	Sequence 5639, Ap	c1962	13.8	0.2	18	1	US-09-029-045-9	Sequence 9, Appl1
c1890	13.8	0.2	17	1	US-09-371-772B-6942	Sequence 6942, Ap	c1963	13.8	0.2	18	1	US-09-174-437-14	Sequence 14, Appl1
c1891	13.8	0.2	17	1	US-09-796-071-6	Sequence 6, Appl1	c1964	13.8	0.2	18	1	US-09-151-467-6	Sequence 6, Appl1
1892	13.8	0.2	17	1	US-09-476-387-557	Sequence 557, App	c1965	13.8	0.2	18	1	US-09-036-599-11	Sequence 11, Appl1
1893	13.8	0.2	17	1	US-09-476-387-656	Sequence 656, App	c1966	13.8	0.2	18	1	US-09-078-402A-15	Sequence 15, Appl1
1894	13.8	0.2	17	1	US-09-476-387-666	Sequence 666, App	c1967	13.8	0.2	18	1	US-09-074-658-37	Sequence 37, Appl1
1895	13.8	0.2	17	1	US-09-401-063-434	Sequence 434, App	c1968	13.8	0.2	18	1	US-09-038-072-2635	Sequence 2635, App
c1896	13.8	0.2	17	1	US-09-827-998-484	Sequence 484, App	c1969	13.8	0.2	18	1	US-09-038-072-2687	Sequence 2687, Ap
1897	13.8	0.2	17	1	US-09-529-812A-3	Sequence 3, Appl1	c1970	13.8	0.2	18	1	US-09-071-433-20	Sequence 20, Appl1
1898	13.8	0.2	17	1	US-09-866-108A-553	Sequence 553, App	c1971	13.8	0.2	18	1	US-09-475-316A-122	Sequence 122, App
1899	13.8	0.2	17	1	US-09-866-108A-554	Sequence 554, App	c1972	13.8	0.2	18	1	US-09-311-260-119	Sequence 119, App
1900	13.8	0.2	17	1	US-09-866-108A-1127	Sequence 1127, Ap	c1973	13.8	0.2	18	1	US-09-593-322-34	Sequence 34, Appl1
c1901	13.8	0.2	17	1	US-09-866-108A-1239	Sequence 1239, Ap	c1974	13.8	0.2	18	1	US-09-251-645-7	Sequence 7, Appl1
c1902	13.8	0.2	17	1	US-09-866-108A-1842	Sequence 1842, Ap	c1975	13.8	0.2	18	1	US-09-594-108-34	Sequence 34, Appl1
c1903	13.8	0.2	17	1	US-09-866-108A-1947	Sequence 1947, Ap	c1976	13.8	0.2	18	1	US-09-577-902-32	Sequence 32, Appl1
1904	13.8	0.2	17	1	US-09-866-108A-2213	Sequence 2213, Ap	c1977	13.8	0.2	18	1	US-09-344-300-34	Sequence 34, Appl1
1905	13.8	0.2	17	1	US-09-866-108A-2214	Sequence 2214, Ap	c1978	13.8	0.2	18	1	US-08-584-040-8406	Sequence 8406, Ap
c1906	13.8	0.2	17	1	US-09-866-108A-2670	Sequence 2670, Ap	c1979	13.8	0.2	18	1	US-08-584-040-8406	Sequence 8406, Ap
1907	13.8	0.2	17	1	US-09-866-108A-2742	Sequence 2742, Ap	c1980	13.8	0.2	18	1	US-08-584-040-8414	Sequence 8414, Ap
c1908	13.8	0.2	17	1	US-09-866-108A-5951	Sequence 5951, Ap	c1981	13.8	0.2	18	1	US-08-686-179A-2	Sequence 2, Appl1
1909	13.8	0.2	17	1	US-09-866-108A-6539	Sequence 6539, Ap	c1982	13.8	0.2	18	1	US-08-679-645-575	Sequence 575, App
c1910	13.8	0.2	17	1	US-09-866-108A-6569	Sequence 6569, Ap	c1983	13.8	0.2	18	1	US-08-679-645-1165	Sequence 1165, App
1911	13.8	0.2	17	1	US-09-866-108A-6859	Sequence 6859, Ap	c1984	13.8	0.2	18	1	US-08-679-645-1185	Sequence 1185, Ap
c1912	13.8	0.2	17	1	US-09-866-108A-7069	Sequence 7069, Ap	c1985	13.8	0.2	18	1	US-09-404-065-10	Sequence 10, Appl1
c1913	13.8	0.2	17	1	US-09-866-108A-7071	Sequence 7071, Ap	c1987	13.8	0.2	18	1	US-09-099-053-9	Sequence 9, Appl1
c1914	13.8	0.2	17	1	US-09-866-108A-7590	Sequence 7590, Ap	c1988	13.8	0.2	18	1	US-09-167-109-1177	Sequence 177, App
1915	13.8	0.2	17	1	US-09-866-108A-7758	Sequence 7758, Ap	c1989	13.8	0.2	18	1	US-09-256-838-6	Sequence 6, Appl1
1917	13.8	0.2	17	1	US-09-866-108A-7801	Sequence 7801, Ap	c1990	13.8	0.2	18	1	US-09-144-367-36	Sequence 36, Appl1
1918	13.8	0.2	17	1	US-09-866-108A-8360	Sequence 8360, Ap	c1991	13.8	0.2	18	1	US-09-250-609-56	Sequence 56, Appl1
1919	13.8	0.2	17	1	US-09-866-108A-8361	Sequence 8361, Ap	c1992	13.8	0.2	18	1	US-09-435-321-9	Sequence 263, App
c1920	13.8	0.2	17	1	US-09-866-108A-8451	Sequence 8451, Ap	c1993	13.8	0.2	18	1	US-09-555-318B-13	Sequence 13, Appl1
1921	13.8	0.2	17	1	US-09-866-108A-9012	Sequence 9012, Ap	c1994	13.8	0.2	18	1	US-09-280-030-42	Sequence 42, Appl1
1922	13.8	0.2	17	1	US-09-866-108A-9013	Sequence 9013, Ap	c1995	13.8	0.2	18	1	US-09-250-611-56	Sequence 56, Appl1
1923	13.8	0.2	17	1	US-09-866-108A-9014	Sequence 9014, Ap	c1996	13.8	0.2	18	1	US-09-573-322-5	Sequence 5, Appl1
1924	13.8	0.2	17	1	US-09-866-108A-9015	Sequence 9015, Ap	c1997	13.8	0.2	18	1	US-09-478-188-28	Sequence 28, Appl1
1925	13.8	0.2	17	1	US-09-866-108A-9016	Sequence 9016, Ap	c1998	13.8	0.2	18	1	US-09-422-978-5122	Sequence 5122, Ap
1926	13.8	0.2	17	1	US-09-866-108A-9254	Sequence 9254, Ap	c1999	13.8	0.2	18	1	US-09-422-978-7190	Sequence 7190, Ap
c1927	13.8	0.2	17	1	US-09-866-108A-9255	Sequence 9255, Ap	2000	13.8	0.2	18	1	US-09-422-978-7310	Sequence 7310, Ap
c1928	13.8	0.2	17	1	US-09-866-108A-9530	Sequence 9530, Ap	2001	13.8	0.2	18	1	US-09-422-978-8353	Sequence 8353, Ap
1929	13.8	0.2	18	1	US-08-487-046-5	Sequence 5, Appl1	2002	13.8	0.2	18	1	US-09-422-978-8353	Sequence 8353, Ap
c1930	13.8	0.2	18	1	US-08-487-046-6	Sequence 6, Appl1	2003	13.8	0.2	18	1	US-09-422-978-10109	Sequence 10109, A
1931	13.8	0.2	18	1	US-08-483-522-5	Sequence 5, Appl1	2004	13.8	0.2	18	1	US-09-422-978-10316	Sequence 10316, A

C2005	13.8	0.2	18	1	US-09-422-978-10643	Sequence 10643, A
C2006	13.8	0.2	18	1	US-09-422-978-11081	Sequence 11081, A
C2007	13.8	0.2	18	1	US-09-422-978-11214	Sequence 11214, A
C2008	13.8	0.2	18	1	US-09-230-652-89	Sequence 89, Appl
C2009	13.8	0.2	18	1	US-09-744-154-9	Sequence 9, Appl
C2010	13.8	0.2	18	1	US-09-686-055A-14	Sequence 14, Appl
C2011	13.8	0.2	18	1	US-09-371-772B-1474	Sequence 1474, Ap
C2012	13.8	0.2	18	1	US-09-371-772B-4062	Sequence 4062, Ap
C2013	13.8	0.2	18	1	US-09-371-772B-4070	Sequence 4070, Ap
C2014	13.8	0.2	18	1	US-09-679-238A-30	Sequence 30, Appl
C2015	13.8	0.2	18	1	US-09-331-568A-8	Sequence 8, Appl
C2016	13.8	0.2	18	1	US-09-981-621-2	Sequence 2, Appl
C2017	13.8	0.2	18	1	US-09-704-640-122	Sequence 122, App
C2018	13.8	0.2	18	1	US-09-495-714C-96	Sequence 96, Appl
C2019	13.8	0.2	18	1	PCT-US92-07815-6	Sequence 263, App
C2020	13.8	0.2	18	1	PCT-US93-11198-263	Sequence 4, Appl
C2021	13.8	0.2	18	1	PCT-US96-01473-4	Sequence 9, Appl
C2022	13.8	0.2	19	1	US-07-985-691-9	Sequence 316, App
C2023	13.8	0.2	19	1	US-08-117-952-316	Sequence 4, Appl
C2024	13.8	0.2	19	1	US-08-987-418A-4	Sequence 7, Appl
C2025	13.8	0.2	19	1	US-09-371-710-7	Sequence 4, Appl
C2026	13.8	0.2	19	1	US-09-343-062-4	Sequence 7, Appl
C2027	13.8	0.2	19	1	US-09-648-386-7	Sequence 4, Appl
C2028	13.8	0.2	19	1	US-09-446-765-1	Sequence 1, Appl
C2029	13.8	0.2	19	1	US-09-564-805-54	Sequence 54, Appl
C2030	13.8	0.2	19	1	US-08-604-986-10	Sequence 10, Appl
C2031	13.8	0.2	19	1	US-09-214-555B-9	Sequence 9, Appl
C2032	13.8	0.2	19	1	US-09-302-681-73	Sequence 73, Appl
C2033	13.8	0.2	19	1	US-09-402-690-15	Sequence 15, Appl
C2034	13.8	0.2	19	1	US-09-470-661A-45	Sequence 40, Appl
C2035	13.8	0.2	19	1	US-09-216-393B-257	Sequence 257, App
C2036	13.8	0.2	19	1	US-09-540-257B-11	Sequence 11, Appl
C2037	13.8	0.2	19	1	US-09-422-978-5607	Sequence 5607, Ap
C2038	13.8	0.2	19	1	US-09-422-978-7196	Sequence 7196, Ap
C2039	13.8	0.2	19	1	US-09-422-978-8453	Sequence 8453, Ap
C2040	13.8	0.2	19	1	US-09-422-978-9771	Sequence 9771, Ap
C2041	13.8	0.2	19	1	US-09-254-776B-42	Sequence 42, Appl
C2042	13.8	0.2	19	1	US-09-672-717-143	Sequence 143, App
C2043	13.8	0.2	19	1	PCT-US91-03680-3	Sequence 3, Appl
C2044	13.8	0.2	19	1	PCT-US94-06311A-21	Sequence 21, Appl
C2045	13.8	0.2	20	1	US-09-536-259-9	Sequence 9, Appl
C2046	13.8	0.2	20	1	US-08-906-156A-87	Sequence 87, Appl
C2047	13.8	0.2	20	1	US-08-031-143B-38	Sequence 38, Appl
C2048	13.8	0.2	20	1	US-08-025-038-4	Sequence 4, Appl
C2049	13.8	0.2	20	1	US-08-271-942A-105	Sequence 105, App
C2050	13.8	0.2	20	1	US-08-104-073-9	Sequence 9, Appl
C2051	13.8	0.2	20	1	US-08-290-936-11	Sequence 11, Appl
C2052	13.8	0.2	20	1	US-08-320-604A-1	Sequence 1, Appl
C2053	13.8	0.2	20	1	US-08-487-141B-16	Sequence 16, Appl
C2054	13.8	0.2	20	1	US-08-271-880A-188	Sequence 188, App
C2055	13.8	0.2	20	1	US-08-535-230A-16	Sequence 16, Appl
C2056	13.8	0.2	20	1	US-08-363-233B-4	Sequence 4, Appl
C2057	13.8	0.2	20	1	US-08-481-633B-3	Sequence 3, Appl
C2058	13.8	0.2	20	1	US-08-480-493A-3	Sequence 3, Appl
C2059	13.8	0.2	20	1	US-08-616-368A-5	Sequence 5, Appl
C2060	13.8	0.2	20	1	US-08-482-638A-3	Sequence 3, Appl
C2061	13.8	0.2	20	1	US-08-559-303B-56	Sequence 56, Appl
C2062	13.8	0.2	20	1	US-08-577-858A-26	Sequence 26, Appl
C2063	13.8	0.2	20	1	US-08-632-575B-5	Sequence 5, Appl
C2064	13.8	0.2	20	1	US-08-485-611A-5	Sequence 5, Appl
C2065	13.8	0.2	20	1	US-08-651-692-9	Sequence 9, Appl
C2066	13.8	0.2	20	1	US-08-852-807-21	Sequence 21, Appl
C2067	13.8	0.2	20	1	US-08-927-551-16	Sequence 16, Appl
C2068	13.8	0.2	20	1	US-08-713-557B-20	Sequence 20, Appl
C2069	13.8	0.2	20	1	US-08-832-658A-4	Sequence 4, Appl
C2070	13.8	0.2	20	1	US-08-912-129A-2	Sequence 2, Appl
C2071	13.8	0.2	20	1	US-08-850-993-7	Sequence 7, Appl
C2072	13.8	0.2	20	1	US-08-997-080-38	Sequence 38, Appl
C2073	13.8	0.2	20	1	US-08-910-408-188	Sequence 188, App
C2074	13.8	0.2	20	1	US-08-997-362-38	Sequence 38, Appl
C2075	13.8	0.2	20	1	US-08-962-284-12	Sequence 12, Appl
C2076	13.8	0.2	20	1	US-08-874-186-20	Sequence 20, Appl
C2077	13.8	0.2	20	1	US-08-873-970-38	Sequence 38, Appl
C2078	13.8	0.2	20	1	US-08-974-180-5	Sequence 5, Appl
C2079	13.8	0.2	20	1	US-08-911-694-75	Sequence 75, Appl
C2080	13.8	0.2	20	1	US-08-755-587-195	Sequence 195, App
C2081	13.8	0.2	20	1	US-09-357-070-23	Sequence 23, Appl
C2082	13.8	0.2	20	1	US-08-779-916A-105	Sequence 105, App
C2083	13.8	0.2	20	1	US-09-106-217-3	Sequence 3, Appl
C2084	13.8	0.2	20	1	US-09-166-186-58	Sequence 58, Appl
C2085	13.8	0.2	20	1	US-09-166-186-196	Sequence 196, App
C2086	13.8	0.2	20	1	US-09-166-186-196	Sequence 196, App
C2087	13.8	0.2	20	1	US-08-988-706-43	Sequence 43, Appl
C2088	13.8	0.2	20	1	US-09-344-914-70	Sequence 70, Appl
C2089	13.8	0.2	20	1	US-09-344-914-71	Sequence 71, Appl
C2090	13.8	0.2	20	1	US-09-418-641-80	Sequence 80, Appl
C2091	13.8	0.2	20	1	US-09-392-350-46	Sequence 46, Appl
C2092	13.8	0.2	20	1	US-09-428-584-18	Sequence 18, Appl
C2093	13.8	0.2	20	1	US-09-054-298-5	Sequence 5, Appl
C2094	13.8	0.2	20	1	US-09-286-704-33	Sequence 33, Appl
C2095	13.8	0.2	20	1	US-09-249-215-188	Sequence 188, App
C2096	13.8	0.2	20	1	US-09-095-855-38	Sequence 38, Appl
C2097	13.8	0.2	20	1	US-09-444-053-70	Sequence 70, Appl
C2098	13.8	0.2	20	1	US-09-433-699-44	Sequence 44, Appl
C2099	13.8	0.2	20	1	US-09-433-699-62	Sequence 62, Appl
C2100	13.8	0.2	20	1	US-09-433-694-25	Sequence 25, Appl
C2101	13.8	0.2	20	1	US-09-513-729B-15	Sequence 15, Appl
C2102	13.8	0.2	20	1	US-09-513-729B-87	Sequence 87, Appl
C2103	13.8	0.2	20	1	US-09-428-219-32	Sequence 32, Appl
C2104	13.8	0.2	20	1	US-09-490-692-121	Sequence 121, App
C2105	13.8	0.2	20	1	US-09-490-692-121	Sequence 121, App
C2106	13.8	0.2	20	1	US-09-488-671-140	Sequence 140, App
C2107	13.8	0.2	20	1	US-09-306-676A-5	Sequence 5, Appl
C2108	13.8	0.2	20	1	US-09-306-676A-6	Sequence 6, Appl
C2109	13.8	0.2	20	1	US-09-517-584A-57	Sequence 57, Appl
C2110	13.8	0.2	20	1	US-09-290-640-77	Sequence 77, Appl
C2111	13.8	0.2	20	1	US-09-175-828-56	Sequence 56, Appl
C2112	13.8	0.2	20	1	US-09-313-932-58	Sequence 58, Appl
C2113	13.8	0.2	20	1	US-09-313-932-196	Sequence 196, App
C2114	13.8	0.2	20	1	US-09-313-932-196	Sequence 196, App
C2115	13.8	0.2	20	1	US-09-313-932-363	Sequence 363, App
C2116	13.8	0.2	20	1	US-09-313-932-477	Sequence 477, App
C2117	13.8	0.2	20	1	US-08-928-213B-41	Sequence 41, Appl
C2118	13.8	0.2	20	1	US-09-021-701-667	Sequence 67, App
C2119	13.8	0.2	20	1	US-09-021-701-668	Sequence 68, App
C2120	13.8	0.2	20	1	US-09-021-701-1052	Sequence 1052, Ap
C2121	13.8	0.2	20	1	US-09-021-701-1053	Sequence 1053, Ap
C2122	13.8	0.2	20	1	US-09-021-701-1054	Sequence 1054, Ap
C2123	13.8	0.2	20	1	US-09-021-701-1055	Sequence 1055, Ap
C2124	13.8	0.2	20	1	US-08-818-655-5	Sequence 5, Appl
C2125	13.8	0.2	20	1	US-09-657-481A-27	Sequence 27, Appl
C2126	13.8	0.2	20	1	US-09-428-583-89	Sequence 89, Appl
C2127	13.8	0.2	20	1	US-09-593-711A-37	Sequence 37, Appl
C2128	13.8	0.2	20	1	US-08-705-347B-38	Sequence 38, Appl
C2129	13.8	0.2	20	1	US-09-284-832-20	Sequence 20, Appl
C2130	13.8	0.2	20	1	US-09-484-617-24	Sequence 24, Appl
C2131	13.8	0.2	20	1	US-09-484-617-139	Sequence 139, App
C2132	13.8	0.2	20	1	US-09-536-094-11	Sequence 11, Appl
C2133	13.8	0.2	20	1	US-09-336-447A-70	Sequence 70, Appl
C2134	13.8	0.2	20	1	US-09-336-447A-71	Sequence 71, Appl
C2135	13.8	0.2	20	1	US-09-324-542-38	Sequence 38, Appl
C2136	13.8	0.2	20	1	US-07-711-303-6	Sequence 6, Appl
C2137	13.8	0.2	20	1	US-07-711-303-13	Sequence 13, Appl
C2138	13.8	0.2	20	1	US-09-434-131A-8	Sequence 8, Appl
C2139	13.8	0.2	20	1	US-09-043-149-17	Sequence 17, Appl
C2140	13.8	0.2	20	1	US-09-716-161A-38	Sequence 38, Appl
C2141	13.8	0.2	20	1	US-09-561-497-43	Sequence 43, Appl
C2142	13.8	0.2	20	1	US-09-561-497-66	Sequence 66, Appl
C2143	13.8	0.2	20	1	US-09-659-991A-41	Sequence 41, Appl
C2144	13.8	0.2	20	1	US-09-308-759B-30	Sequence 30, Appl
C2145	13.8	0.2	20	1	US-09-851-520-55	Sequence 55, Appl
C2146	13.8	0.2	20	1	US-09-205-426-38	Sequence 38, Appl
C2147	13.8	0.2	20	1	US-09-634-934-20	Sequence 20, Appl
C2148	13.8	0.2	20	1	US-09-851-896-33	Sequence 33, Appl
C2149	13.8	0.2	20	1	US-09-254-465A-17	Sequence 17, Appl
C2150	13.8	0.2	20	1	US-09-200-643-38	Sequence 38, Appl



c2151	13.8	0.2	20	1	US-09-689-291A-12	Sequence 12, Appl	c2224	13.8	0.2	21	1	US-08-173-489C-117	Sequence 117, App
c2152	13.8	0.2	20	1	US-08-744-481A-42	Sequence 42, Appl	c2225	13.8	0.2	21	1	US-09-422-978-10694	Sequence 10694, A
c2153	13.8	0.2	20	1	US-09-661-753-2	Sequence 2, Appl1	c2226	13.8	0.2	21	1	PCT-US94-06661-3	Sequence 3, Appl1
c2154	13.8	0.2	20	1	US-09-907-843-62	Sequence 62, Appl1	c2227	13.8	0.2	21	1	PCT-US96-09440-9	Sequence 9, Appl1
c2155	13.8	0.2	20	1	US-09-907-843-65	Sequence 65, Appl1	c2228	13.8	0.2	21	1	US-07-858-124-6	Sequence 6, Appl1
c2156	13.8	0.2	20	1	US-09-676-610B-4	Sequence 4, Appl1	c2229	13.8	0.2	21	1	US-08-071-601-12	Sequence 12, Appl1
c2157	13.8	0.2	20	1	US-09-640-101-33	Sequence 33, Appl1	c2230	13.8	0.2	21	1	US-08-185-301-4	Sequence 4, Appl1
c2158	13.8	0.2	20	1	US-09-517-647B-241	Sequence 241, Appl	c2231	13.8	0.2	21	1	US-08-358-901-8	Sequence 8, Appl1
c2159	13.8	0.2	20	1	US-09-300-008B-26	Sequence 26, Appl1	c2232	13.8	0.2	21	1	US-08-566-347-8	Sequence 8, Appl1
c2160	13.8	0.2	20	1	US-09-657-453A-67	Sequence 67, Appl1	c2233	13.8	0.2	21	1	US-08-122-795B-9	Sequence 9, Appl1
c2161	13.8	0.2	20	1	US-09-918-686-54	Sequence 54, Appl1	c2234	13.8	0.2	21	1	US-08-619-596-6	Sequence 6, Appl1
c2162	13.8	0.2	20	1	US-09-199-542B-5	Sequence 5, Appl1	c2235	13.8	0.2	21	1	US-08-588-821-46	Sequence 46, Appl1
c2163	13.8	0.2	20	1	US-09-527-030G-349	Sequence 349, Appl	c2236	13.8	0.2	21	1	US-08-525-652A-119	Sequence 119, App
c2164	13.8	0.2	20	1	US-09-725-265-39	Sequence 39, Appl1	c2237	13.8	0.2	21	1	US-08-632-598-28	Sequence 28, Appl1
c2165	13.8	0.2	20	1	US-09-659-845A-147	Sequence 147, App	c2238	13.8	0.2	21	1	US-08-693-853A-127	Sequence 8, Appl1
c2166	13.8	0.2	20	1	US-09-657-346A-104	Sequence 104, App	c2239	13.8	0.2	21	1	US-08-294-424-38	Sequence 38, Appl1
c2167	13.8	0.2	20	1	US-09-305-839-5	Sequence 5, Appl1	c2240	13.8	0.2	21	1	US-08-915-214-46	Sequence 46, Appl1
c2168	13.8	0.2	20	1	US-09-422-978-4151	Sequence 4151, Ap	c2241	13.8	0.2	21	1	US-08-726-575A-3	Sequence 3, Appl1
c2169	13.8	0.2	20	1	US-09-422-978-6065	Sequence 5517, Ap	c2242	13.8	0.2	21	1	US-08-621-100-12	Sequence 12, Appl1
c2170	13.8	0.2	20	1	US-09-422-978-7498	Sequence 6065, Ap	c2243	13.8	0.2	21	1	US-08-632-598-28	Sequence 28, Appl1
c2171	13.8	0.2	20	1	US-09-422-978-6799	Sequence 6799, Ap	c2244	13.8	0.2	21	1	US-08-480-020B-12	Sequence 12, Appl1
c2172	13.8	0.2	20	1	US-09-422-978-7498	Sequence 7498, Ap	c2245	13.8	0.2	21	1	US-08-480-020B-13	Sequence 13, Appl1
c2173	13.8	0.2	20	1	US-09-422-978-8813	Sequence 8813, Ap	c2246	13.8	0.2	21	1	US-09-005-534-16	Sequence 46, Appl1
c2174	13.8	0.2	20	1	US-09-060-299-61	Sequence 61, Appl1	c2247	13.8	0.2	21	1	US-09-910-618-13	Sequence 13, Appl1
c2175	13.8	0.2	20	1	US-09-060-299-391	Sequence 391, App	c2248	13.8	0.2	21	1	US-08-822-028-47	Sequence 47, Appl1
c2176	13.8	0.2	20	1	US-09-705-267A-31	Sequence 31, Appl1	c2249	13.8	0.2	21	1	US-08-822-028-48	Sequence 48, Appl1
c2177	13.8	0.2	20	1	US-09-402-523A-61	Sequence 61, Appl1	c2250	13.8	0.2	21	1	US-08-822-028-49	Sequence 49, Appl1
c2178	13.8	0.2	20	1	US-09-402-923A-391	Sequence 391, App	c2251	13.8	0.2	21	1	US-08-899-768-31	Sequence 31, Appl1
c2179	13.8	0.2	20	1	US-09-198-452A-1354	Sequence 1354, Ap	c2252	13.8	0.2	21	1	US-08-445-463B-94	Sequence 94, Appl1
c2180	13.8	0.2	20	1	US-09-198-452A-1518	Sequence 1518, Ap	c2253	13.8	0.2	21	1	US-08-445-463B-95	Sequence 95, Appl1
c2181	13.8	0.2	20	1	US-09-198-452A-2177	Sequence 2177, Ap	c2254	13.8	0.2	21	1	US-09-106-217-10	Sequence 10, Appl1
c2182	13.8	0.2	20	1	US-09-198-452A-2793	Sequence 2793, Ap	c2255	13.8	0.2	21	1	US-09-009-913-127	Sequence 127, App
c2183	13.8	0.2	20	1	US-09-198-452A-2814	Sequence 2814, Ap	c2256	13.8	0.2	21	1	US-08-445-464C-94	Sequence 94, Appl1
c2184	13.8	0.2	20	1	US-09-198-452A-2863	Sequence 2863, Ap	c2257	13.8	0.2	21	1	US-08-445-464C-95	Sequence 95, Appl1
c2185	13.8	0.2	20	1	US-09-198-452A-3031	Sequence 3031, Ap	c2258	13.8	0.2	21	1	US-08-545-809A-85	Sequence 85, Appl1
c2186	13.8	0.2	20	1	US-09-198-452A-3229	Sequence 3229, Ap	c2259	13.8	0.2	21	1	US-08-929-322-23	Sequence 23, Appl1
c2187	13.8	0.2	20	1	US-09-198-452A-3792	Sequence 3792, Ap	c2260	13.8	0.2	21	1	US-08-905-359A-15	Sequence 15, Appl1
c2188	13.8	0.2	20	1	US-09-198-452A-3806	Sequence 3806, Ap	c2261	13.8	0.2	21	1	US-09-217-499-15	Sequence 15, Appl1
c2189	13.8	0.2	20	1	US-09-198-452A-4100	Sequence 4100, Ap	c2262	13.8	0.2	21	1	US-08-974-548A-444	Sequence 444, App
c2190	13.8	0.2	20	1	US-09-198-452A-4101	Sequence 4101, Ap	c2263	13.8	0.2	21	1	US-09-353-556-5	Sequence 5, Appl1
c2191	13.8	0.2	20	1	US-09-198-452A-4289	Sequence 4289, Ap	c2264	13.8	0.2	21	1	US-08-479-285-47	Sequence 47, Appl1
c2192	13.8	0.2	20	1	US-09-198-452A-4674	Sequence 4674, Ap	c2265	13.8	0.2	21	1	US-08-943-731-336	Sequence 336, App
c2193	13.8	0.2	20	1	US-09-198-452A-4963	Sequence 4963, Ap	c2266	13.8	0.2	21	1	US-08-973-124-270	Sequence 270, App
c2194	13.8	0.2	20	1	US-09-198-452A-5344	Sequence 5344, Ap	c2267	13.8	0.2	21	1	US-08-973-124-270	Sequence 270, App
c2195	13.8	0.2	20	1	US-09-198-452A-5420	Sequence 5420, Ap	c2268	13.8	0.2	21	1	US-08-910-322-13	Sequence 13, Appl1
c2196	13.8	0.2	20	1	US-09-198-452A-5800	Sequence 5800, Ap	c2269	13.8	0.2	21	1	US-09-231-240-28	Sequence 28, Appl1
c2197	13.8	0.2	20	1	US-09-198-452A-5852	Sequence 5852, Ap	c2270	13.8	0.2	21	1	US-08-943-731-336	Sequence 336, App
c2198	13.8	0.2	20	1	US-09-198-452A-5937	Sequence 5937, Ap	c2271	13.8	0.2	21	1	US-08-484-939A-12	Sequence 12, Appl1
c2199	13.8	0.2	20	1	US-09-198-452A-5947	Sequence 5947, Ap	c2272	13.8	0.2	21	1	US-08-484-939A-13	Sequence 13, Appl1
c2200	13.8	0.2	20	1	US-09-198-452A-6635	Sequence 6635, Ap	c2273	13.8	0.2	21	1	US-09-354-231B-21	Sequence 21, Appl1
c2201	13.8	0.2	20	1	US-09-679-299A-147	Sequence 147, App	c2274	13.8	0.2	21	1	US-09-397-166-37	Sequence 37, Appl1
c2202	13.8	0.2	20	1	US-09-081-385-82	Sequence 85, Appl1	c2275	13.8	0.2	21	1	US-09-543-084A-5	Sequence 5, Appl1
c2203	13.8	0.2	20	1	US-09-081-385-85	Sequence 85, Appl1	c2276	13.8	0.2	21	1	US-09-495-797-7	Sequence 7, Appl1
c2204	13.8	0.2	20	1	US-09-081-385-123	Sequence 123, App	c2277	13.8	0.2	21	1	US-09-593-012-17	Sequence 17, Appl1
c2205	13.8	0.2	20	1	US-09-780-045-105	Sequence 105, App	c2278	13.8	0.2	21	1	US-09-593-012-26	Sequence 26, Appl1
c2206	13.8	0.2	20	1	US-09-689-065B-11	Sequence 11, Appl1	c2279	13.8	0.2	21	1	US-09-593-012-32	Sequence 32, Appl1
c2207	13.8	0.2	20	1	US-09-112-580-102	Sequence 102, App	c2280	13.8	0.2	21	1	US-09-593-012-41	Sequence 41, Appl1
c2208	13.8	0.2	20	1	US-09-526-193A-105	Sequence 105, App	c2281	13.8	0.2	21	1	US-09-099-093-24	Sequence 24, Appl1
c2209	13.8	0.2	20	1	US-09-989-002-7	Sequence 7, Appl1	c2282	13.8	0.2	21	1	US-08-936-107A-26	Sequence 26, Appl1
c2210	13.8	0.2	20	1	US-09-907-794A-125	Sequence 125, App	c2283	13.8	0.2	21	1	US-09-128-602B-21	Sequence 21, Appl1
c2211	13.8	0.2	20	1	US-09-907-794A-125	Sequence 125, App	c2284	13.8	0.2	21	1	US-09-384-472-12	Sequence 12, Appl1
c2212	13.8	0.2	20	1	US-09-665-615B-77	Sequence 77, Appl1	c2285	13.8	0.2	21	1	US-08-044-857D-94	Sequence 94, Appl1
c2213	13.8	0.2	20	1	US-09-860-473-76	Sequence 76, Appl1	c2286	13.8	0.2	21	1	US-08-044-857D-95	Sequence 95, Appl1
c2214	13.8	0.2	20	1	US-09-905-125A-125	Sequence 125, App	c2287	13.8	0.2	21	1	US-08-912-951-211	Sequence 211, App
c2215	13.8	0.2	20	1	US-09-980-052-69	Sequence 69, Appl1	c2288	13.8	0.2	21	1	US-08-912-951-212	Sequence 212, App
c2216	13.8	0.2	20	1	PCT-US94-02891-38	Sequence 125, App	c2289	13.8	0.2	21	1	US-09-470-661A-15	Sequence 15, Appl1
c2217	13.8	0.2	20	1	PCT-US94-06331A-60	Sequence 38, Appl1	c2290	13.8	0.2	21	1	US-09-384-472-13	Sequence 13, Appl1
c2218	13.8	0.2	20	1	PCT-US96-08604-105	Sequence 105, App	c2291	13.8	0.2	21	1	US-09-422-978-7896	Sequence 7896, Ap
c2219	13.8	0.2	20	1	PCT-US96-09388-16	Sequence 16, Appl1	c2292	13.8	0.2	21	1	US-09-422-978-8974	Sequence 8974, Ap
c2220	13.8	0.2	20	1	5219727-9	Patent No. 5219727	c2293	13.8	0.2	21	1	US-09-422-978-9102	Sequence 9102, Ap
c2221	13.8	0.2	21	1	US-09-422-978-9563	Sequence 9563, Ap	c2295	13.8	0.2	21	1	US-09-422-978-9319	Sequence 9319, Ap
c2222	13.8	0.2	21	1	US-08-076-090-3	Sequence 3, Appl1	c2296	13.8	0.2	21	1	US-09-422-978-11523	Sequence 11523, A



C2297	13.8	0.2	21	1	US-09-422-978-11631	Sequence 11631, A	C2370	13.6	0.2	20	1	US-08-384-490-7	Sequence 7, Appl
C2298	13.8	0.2	21	1	US-09-460-548B-15	Sequence 15, Appl	C2371	13.6	0.2	20	1	US-08-106-802-13	Sequence 13, Appl
C2299	13.8	0.2	21	1	US-09-402-181B-444	Sequence 444, App	C2372	13.6	0.2	20	1	US-08-379-078-353	Sequence 353, App
C2300	13.8	0.2	21	1	US-09-721-456-444	Sequence 444, App	C2373	13.6	0.2	20	1	US-08-502-185-13	Sequence 13, Appl
C2301	13.8	0.2	21	1	US-09-674-826B-11	Sequence 11, Appl	C2374	13.6	0.2	20	1	US-08-502-185-25	Sequence 25, Appl
C2302	13.8	0.2	21	1	US-09-503-653A-47	Sequence 47, Appl	C2375	13.6	0.2	20	1	US-08-398-945-13	Sequence 13, Appl
C2303	13.8	0.2	21	1	US-09-503-653A-48	Sequence 48, Appl	C2376	13.6	0.2	20	1	US-08-398-945-25	Sequence 25, Appl
C2304	13.8	0.2	21	1	US-09-995-297-21	Sequence 21, Appl	C2377	13.6	0.2	20	1	US-08-233-009-17	Sequence 17, Appl
C2305	13.8	0.2	21	1	US-09-382-552-221	Sequence 221, App	C2378	13.6	0.2	20	1	US-08-261-822A-55	Sequence 55, Appl
C2306	13.8	0.2	21	1	PCT-US94-03437-94	Sequence 94, Appl	C2379	13.6	0.2	20	1	US-08-484-138-36	Sequence 36, Appl
C2307	13.8	0.2	21	1	PCT-US94-03437-95	Sequence 95, Appl	C2380	13.6	0.2	20	1	US-08-501-779-13	Sequence 13, Appl
C2308	13.8	0.2	21	1	PCT-US94-09963A-9	Sequence 9, Appl	C2381	13.6	0.2	20	1	US-08-501-779-25	Sequence 25, Appl
C2309	13.8	0.2	21	1	PCT-US96-08014-270	Sequence 270, App	C2382	13.6	0.2	20	1	US-08-195-152-8	Sequence 8, Appl
C2310	13.8	0.2	24	1	US-08-200-807-3	Sequence 3, Appl	C2383	13.6	0.2	20	1	US-08-363-585-38	Sequence 38, Appl
C2311	13.8	0.2	29	1	US-08-488-305A-3	Sequence 3, Appl	C2384	13.6	0.2	20	1	US-08-363-585-40	Sequence 40, Appl
C2312	13.8	0.2	29	1	US-08-227-476-5	Sequence 5, Appl	C2385	13.6	0.2	20	1	US-08-363-585-42	Sequence 42, Appl
C2313	13.8	0.2	30	1	US-08-480-784-41	Sequence 41, Appl	C2386	13.6	0.2	20	1	US-08-363-585-44	Sequence 44, Appl
C2314	13.8	0.2	30	1	US-08-483-553-41	Sequence 41, Appl	C2387	13.6	0.2	20	1	US-08-363-585-46	Sequence 46, Appl
C2315	13.8	0.2	30	1	US-08-487-002-41	Sequence 41, Appl	C2388	13.6	0.2	20	1	US-08-356-287-23	Sequence 23, Appl
C2316	13.8	0.2	30	1	US-08-483-554B-41	Sequence 41, Appl	C2389	13.6	0.2	20	1	US-08-413-118-28	Sequence 28, Appl
C2317	13.8	0.2	30	1	US-08-488-011B-41	Sequence 41, Appl	C2390	13.6	0.2	20	1	US-08-271-880A-172	Sequence 172, App
C2318	13.8	0.2	30	1	US-08-850-727-41	Sequence 41, Appl	C2391	13.6	0.2	20	1	US-08-271-880A-189	Sequence 189, App
C2319	13.8	0.2	30	1	PCT-US95-10202-41	Sequence 41, Appl	C2392	13.6	0.2	20	1	US-08-535-230A-4	Sequence 4, Appl
C2320	13.8	0.2	30	1	PCT-US95-10203-41	Sequence 41, Appl	C2393	13.6	0.2	20	1	US-08-501-713-13	Sequence 13, Appl
C2321	13.8	0.2	30	1	PCT-US95-10220-41	Sequence 41, Appl	C2394	13.6	0.2	20	1	US-08-501-713-25	Sequence 25, Appl
C2322	13.8	0.2	33	1	US-08-465-384-4	Sequence 4, Appl	C2395	13.6	0.2	20	1	US-08-117-083-2	Sequence 2, Appl
C2323	13.6	0.2	20	1	US-08-146-504-16	Sequence 16, Appl	C2396	13.6	0.2	20	1	US-08-378-660-13	Sequence 13, Appl
C2324	13.6	0.2	20	1	US-08-379-593-5	Sequence 5, Appl	C2397	13.6	0.2	20	1	US-08-378-660-25	Sequence 25, Appl
C2325	13.6	0.2	20	1	US-08-725-976-16	Sequence 16, Appl	C2398	13.6	0.2	20	1	US-08-689-936-8	Sequence 8, Appl
C2326	13.6	0.2	20	1	US-08-997-080-83	Sequence 83, Appl	C2399	13.6	0.2	20	1	US-08-459-983-7	Sequence 7, Appl
C2327	13.6	0.2	20	1	US-08-997-362-83	Sequence 83, Appl	C2400	13.6	0.2	20	1	US-08-224-491-5	Sequence 5, Appl
C2328	13.6	0.2	20	1	US-08-965-780-1	Sequence 1, Appl	C2401	13.6	0.2	20	1	US-08-484-304-5	Sequence 5, Appl
C2329	13.6	0.2	20	1	US-08-873-970-83	Sequence 83, Appl	C2402	13.6	0.2	20	1	US-08-689-935-8	Sequence 8, Appl
C2330	13.6	0.2	20	1	US-08-765-340-96	Sequence 96, Appl	C2403	13.6	0.2	20	1	US-08-224-657-5	Sequence 5, Appl
C2331	13.6	0.2	20	1	US-09-095-855-83	Sequence 83, Appl	C2404	13.6	0.2	20	1	US-08-692-725-8	Sequence 8, Appl
C2332	13.6	0.2	20	1	US-09-407-675-1	Sequence 1, Appl	C2405	13.6	0.2	20	1	US-08-475-663-5	Sequence 5, Appl
C2333	13.6	0.2	20	1	US-09-250-075-1	Sequence 1, Appl	C2406	13.6	0.2	20	1	US-08-207-792-5	Sequence 5, Appl
C2334	13.6	0.2	20	1	US-09-173-936B-14	Sequence 14, Appl	C2407	13.6	0.2	20	1	US-08-487-412-21	Sequence 21, Appl
C2335	13.6	0.2	20	1	US-09-454-704A-13	Sequence 13, Appl	C2408	13.6	0.2	20	1	US-08-709-409-5	Sequence 5, Appl
C2336	13.6	0.2	20	1	US-09-324-542-83	Sequence 83, Appl	C2409	13.6	0.2	20	1	US-08-257-073-1	Sequence 1, Appl
C2337	13.6	0.2	20	1	US-09-205-426-83	Sequence 83, Appl	C2410	13.6	0.2	20	1	US-08-303-775-5	Sequence 5, Appl
C2338	13.6	0.2	20	1	US-09-619-103-26	Sequence 26, Appl	C2411	13.6	0.2	20	1	US-08-458-101-5	Sequence 5, Appl
C2339	13.6	0.2	20	1	US-09-726-096A-1	Sequence 1, Appl	C2412	13.6	0.2	20	1	US-08-753-147-70	Sequence 70, Appl
C2340	13.6	0.2	20	1	US-09-603-830-55	Sequence 55, Appl	C2413	13.6	0.2	20	1	US-08-531-556-116	Sequence 116, App
C2341	13.6	0.2	20	1	US-09-976-978A-55	Sequence 55, Appl	C2414	13.6	0.2	20	1	US-08-371-001-10	Sequence 10, Appl
C2342	13.6	0.2	20	1	US-09-344-260A-10	Sequence 10, Appl	C2415	13.6	0.2	20	1	US-08-640-672-8	Sequence 8, Appl
C2343	13.6	0.2	20	1	US-09-961-949A-55	Sequence 55, Appl	C2416	13.6	0.2	20	1	US-08-729-447-7	Sequence 7, Appl
C2344	13.6	0.2	20	1	US-09-966-491A-55	Sequence 55, Appl	C2417	13.6	0.2	20	1	US-08-110-691A-35	Sequence 35, Appl
C2345	13.6	0.2	20	1	US-09-957-313A-55	Sequence 55, Appl	C2418	13.6	0.2	20	1	US-08-343-881A-9	Sequence 9, Appl
C2346	13.6	0.2	20	1	US-09-966-312-55	Sequence 55, Appl	C2419	13.6	0.2	20	1	US-08-501-626-13	Sequence 13, Appl
C2347	13.6	0.2	20	1	US-09-975-062A-55	Sequence 55, Appl	C2420	13.6	0.2	20	1	US-08-501-626-25	Sequence 25, Appl
C2348	13.6	0.2	20	1	US-09-976-971A-55	Sequence 55, Appl	C2421	13.6	0.2	20	1	US-08-410-779B-60	Sequence 60, Appl
C2349	13.6	0.2	20	1	PCT-US93-07603-6	Sequence 6, Appl	C2422	13.6	0.2	20	1	US-08-501-356-13	Sequence 13, Appl
C2350	13.6	0.2	20	1	US-09-808-358-18	Sequence 18, Appl	C2423	13.6	0.2	20	1	US-08-501-356-25	Sequence 25, Appl
C2351	13.6	0.2	20	1	US-09-808-358-44	Sequence 44, Appl	C2424	13.6	0.2	20	1	US-08-560-231-17	Sequence 17, Appl
C2352	13.6	0.2	20	1	US-07-752-101A-27	Sequence 27, Appl	C2425	13.6	0.2	20	1	US-08-688-088-5	Sequence 5, Appl
C2353	13.6	0.2	20	1	US-08-036-217-5	Sequence 5, Appl	C2426	13.6	0.2	20	1	US-08-684-998A-8	Sequence 8, Appl
C2354	13.6	0.2	20	1	US-07-641-143B-3	Sequence 3, Appl	C2427	13.6	0.2	20	1	US-08-184-009-5	Sequence 5, Appl
C2355	13.6	0.2	20	1	US-08-004-552-1	Sequence 1, Appl	C2428	13.6	0.2	20	1	US-08-577-858A-8	Sequence 8, Appl
C2356	13.6	0.2	20	1	US-08-105-483-5	Sequence 5, Appl	C2429	13.6	0.2	20	1	US-08-790-963-50	Sequence 50, Appl
C2357	13.6	0.2	20	1	US-08-073-962-21	Sequence 21, Appl	C2430	13.6	0.2	20	1	US-08-753-879A-12	Sequence 12, Appl
C2358	13.6	0.2	20	1	US-07-714-687-5	Sequence 5, Appl	C2431	13.6	0.2	20	1	US-08-486-969-5	Sequence 5, Appl
C2359	13.6	0.2	20	1	US-08-150-531-26	Sequence 26, Appl	C2432	13.6	0.2	20	1	US-08-992-726-8	Sequence 8, Appl
C2360	13.6	0.2	20	1	US-08-220-151-28	Sequence 28, Appl	C2433	13.6	0.2	20	1	US-08-117-952-317	Sequence 317, App
C2361	13.6	0.2	20	1	US-08-281-082A-2	Sequence 2, Appl	C2434	13.6	0.2	20	1	US-08-578-551-26	Sequence 26, Appl
C2362	13.6	0.2	20	1	US-08-242-664-36	Sequence 36, Appl	C2435	13.6	0.2	20	1	US-08-887-365-29	Sequence 29, Appl
C2363	13.6	0.2	20	1	US-07-665-960A-13	Sequence 13, Appl	C2436	13.6	0.2	20	1	US-08-468-037A-17	Sequence 17, Appl
C2364	13.6	0.2	20	1	US-07-955-718-9	Sequence 9, Appl	C2437	13.6	0.2	20	1	US-08-626-169-19	Sequence 19, Appl
C2365	13.6	0.2	20	1	US-07-955-718-11	Sequence 11, Appl	C2438	13.6	0.2	20	1	US-08-417-210A-5	Sequence 5, Appl
C2366	13.6	0.2	20	1	US-08-379-081B-353	Sequence 353, App	C2439	13.6	0.2	20	1	US-08-468-819-29	Sequence 29, Appl
C2367	13.6	0.2	20	1	US-08-124-290-3	Sequence 3, Appl	C2440	13.6	0.2	20	1	US-08-468-819-37	Sequence 37, Appl
C2368	13.6	0.2	20	1	US-08-349-696-17	Sequence 17, Appl	C2441	13.6	0.2	20	1	US-08-468-819-45	Sequence 45, Appl
C2369	13.6	0.2	20	1	US-08-587-209-8	Sequence 8, Appl	C2442	13.6	0.2	20	1	US-08-468-819-65	Sequence 65, Appl

2443	13.6	0.2	20	1	US-08-471-973A-17	Sequence 17, Appl	2516	13.6	0.2	20	1	US-09-288-461-47	Sequence 47, Appl
c2444	13.6	0.2	20	1	US-08-869-296A-20	Sequence 20, Appl	c2517	13.6	0.2	20	1	US-09-444-053-34	Sequence 34, Appl
2445	13.6	0.2	20	1	US-08-692-787-43	Sequence 43, Appl	c2518	13.6	0.2	20	1	US-09-080-704A-17	Sequence 17, Appl
2446	13.6	0.2	20	1	US-08-668-448-5	Sequence 5, Appl1	c2519	13.6	0.2	20	1	US-09-435-226-56	Sequence 56, Appl
2447	13.6	0.2	20	1	US-08-540-804-22	Sequence 22, Appl	2520	13.6	0.2	20	1	US-09-490-692-67	Sequence 67, Appl
2448	13.6	0.2	20	1	US-08-218-265-22	Sequence 22, Appl	2521	13.6	0.2	20	1	US-09-490-692-68	Sequence 68, Appl
c2449	13.6	0.2	20	1	US-08-529-878B-31	Sequence 31, Appl	c2522	13.6	0.2	20	1	US-09-490-692-72	Sequence 72, Appl
c2450	13.6	0.2	20	1	US-08-931-072A-39	Sequence 39, Appl	c2523	13.6	0.2	20	1	US-09-490-692-135	Sequence 125, App
c2451	13.6	0.2	20	1	US-08-458-356-5	Sequence 5, Appl1	2524	13.6	0.2	20	1	US-09-280-805-147	Sequence 147, App
c2452	13.6	0.2	20	1	US-08-875-377-2	Sequence 2, Appl1	c2525	13.6	0.2	20	1	US-09-075-501-5	Sequence 5, Appl1
2453	13.6	0.2	20	1	US-08-975-211-29	Sequence 29, Appl	2526	13.6	0.2	20	1	US-09-517-584A-73	Sequence 73, Appl
2454	13.6	0.2	20	1	US-08-756-806A-44	Sequence 44, Appl	2527	13.6	0.2	20	1	US-09-046-894-55	Sequence 55, Appl
c2455	13.6	0.2	20	1	US-08-756-806A-59	Sequence 59, Appl	2528	13.6	0.2	20	1	US-09-408-257-26	Sequence 26, Appl
2456	13.6	0.2	20	1	US-09-044-506A-14	Sequence 14, Appl	2529	13.6	0.2	20	1	US-09-092-077-31	Sequence 31, Appl
2457	13.6	0.2	20	1	US-08-465-880-22	Sequence 22, Appl	c2530	13.6	0.2	20	1	US-09-092-077-33	Sequence 33, Appl
c2458	13.6	0.2	20	1	US-08-848-840A-20	Sequence 20, Appl	2531	13.6	0.2	20	1	US-09-101-886B-44	Sequence 44, Appl
c2459	13.6	0.2	20	1	US-08-703-136-13	Sequence 13, Appl	c2532	13.6	0.2	20	1	US-09-101-886B-89	Sequence 89, Appl1
2460	13.6	0.2	20	1	US-08-910-408-172	Sequence 172, App	c2533	13.6	0.2	20	1	US-09-413-304-9	Sequence 9, Appl1
2461	13.6	0.2	20	1	US-08-863-639A-72	Sequence 189, App	2534	13.6	0.2	20	1	US-09-244-794A-31	Sequence 31, Appl
c2462	13.6	0.2	20	1	US-08-863-639A-93	Sequence 72, Appl	2535	13.6	0.2	20	1	US-09-590-393-22	Sequence 204, App
2463	13.6	0.2	20	1	US-08-837-201C-63	Sequence 93, Appl	2536	13.6	0.2	20	1	US-09-262-773-204	Sequence 17, Appl
2464	13.6	0.2	20	1	US-08-837-201C-75	Sequence 63, Appl	c2538	13.6	0.2	20	1	US-09-313-932-17	Sequence 22, Appl
c2466	13.6	0.2	20	1	US-08-837-201C-75	Sequence 75, Appl	2539	13.6	0.2	20	1	US-09-313-932-22	Sequence 398, App
c2467	13.6	0.2	20	1	US-08-471-025-5	Sequence 5, Appl1	c2540	13.6	0.2	20	1	US-08-996-069A-15	Sequence 15, Appl
c2468	13.6	0.2	20	1	US-08-658-665-5	Sequence 8, Appl1	c2541	13.6	0.2	20	1	US-08-996-069A-17	Sequence 17, Appl
2469	13.6	0.2	20	1	US-09-190-982-26	Sequence 26, Appl	2542	13.6	0.2	20	1	US-09-038-637-106	Sequence 106, App
c2470	13.6	0.2	20	1	US-09-426-568-11	Sequence 11, Appl	2543	13.6	0.2	20	1	US-09-290-577-5	Sequence 5, Appl1
c2471	13.6	0.2	20	1	US-08-917-653-1	Sequence 1, Appl1	2544	13.6	0.2	20	1	US-09-290-577-22	Sequence 22, Appl
2472	13.6	0.2	20	1	US-09-035-357-17	Sequence 17, Appl	c2545	13.6	0.2	20	1	US-09-371-774-50	Sequence 50, Appl
2473	13.6	0.2	20	1	US-08-809-999D-4	Sequence 4, Appl	2546	13.6	0.2	20	1	US-09-560-594-54	Sequence 54, Appl
2474	13.6	0.2	20	1	US-08-521-872-22	Sequence 22, Appl	c2547	13.6	0.2	20	1	US-09-021-701-351	Sequence 351, App
c2475	13.6	0.2	20	1	US-08-473-446-28	Sequence 28, Appl	c2548	13.6	0.2	20	1	US-09-021-701-353	Sequence 353, App
2476	13.6	0.2	20	1	US-09-069-637-4	Sequence 4, Appl1	2549	13.6	0.2	20	1	US-09-021-701-399	Sequence 399, App
c2477	13.6	0.2	20	1	US-09-366-257-35	Sequence 35, Appl	2550	13.6	0.2	20	1	US-09-021-701-400	Sequence 400, App
2478	13.6	0.2	20	1	US-08-979-269-11	Sequence 16, Appl	2551	13.6	0.2	20	1	US-09-021-701-404	Sequence 404, App
2479	13.6	0.2	20	1	US-08-742-877-11	Sequence 11, Appl	c2552	13.6	0.2	20	1	US-09-021-701-512	Sequence 512, App
2480	13.6	0.2	20	1	US-09-106-217-7	Sequence 7, Appl1	2553	13.6	0.2	20	1	US-09-021-701-550	Sequence 550, App
c2481	13.6	0.2	20	1	US-09-132-652-23	Sequence 23, Appl	c2554	13.6	0.2	20	1	US-09-021-701-663	Sequence 663, App
c2482	13.6	0.2	20	1	US-09-111-752-2	Sequence 2, Appl	c2555	13.6	0.2	20	1	US-09-021-701-664	Sequence 664, App
2483	13.6	0.2	20	1	US-08-696-372A-3	Sequence 3, Appl1	c2556	13.6	0.2	20	1	US-09-021-701-673	Sequence 673, App
c2484	13.6	0.2	20	1	US-08-945-056-14	Sequence 14, Appl	2557	13.6	0.2	20	1	US-09-043-303-8	Sequence 8, Appl1
2485	13.6	0.2	20	1	US-09-166-186-17	Sequence 17, Appl	2558	13.6	0.2	20	1	US-08-875-847B-29	Sequence 29, Appl
c2486	13.6	0.2	20	1	US-09-166-186-12	Sequence 12, Appl	2559	13.6	0.2	20	1	US-09-007-005-31	Sequence 31, Appl
c2487	13.6	0.2	20	1	US-08-961-469A-28	Sequence 28, Appl	c2560	13.6	0.2	20	1	US-09-487-445-47	Sequence 47, Appl
c2488	13.6	0.2	20	1	US-09-009-913-259	Sequence 259, App	2561	13.6	0.2	20	1	US-09-657-481A-37	Sequence 37, Appl
2489	13.6	0.2	20	1	US-09-164-907-19	Sequence 19, Appl	c2562	13.6	0.2	20	1	US-09-377-303-76	Sequence 76, Appl
c2490	13.6	0.2	20	1	US-09-143-214-44	Sequence 44, Appl	c2563	13.6	0.2	20	1	US-08-090-363-12	Sequence 12, Appl
c2491	13.6	0.2	20	1	US-09-143-214-59	Sequence 59, Appl	2564	13.6	0.2	20	1	US-09-247-193-31	Sequence 31, Appl
c2492	13.6	0.2	20	1	US-08-621-841-45	Sequence 45, Appl	2565	13.6	0.2	20	1	US-09-487-368A-131	Sequence 131, App
2493	13.6	0.2	20	1	US-09-344-914-68	Sequence 68, Appl	2566	13.6	0.2	20	1	US-08-943-731-513	Sequence 513, App
c2494	13.6	0.2	20	1	US-09-344-914-74	Sequence 74, Appl	c2567	13.6	0.2	20	1	US-08-460-735-5	Sequence 5, Appl1
c2495	13.6	0.2	20	1	US-09-344-914-75	Sequence 75, Appl	c2568	13.6	0.2	20	1	US-09-489-866A-49	Sequence 49, Appl
c2496	13.6	0.2	20	1	US-09-344-914-76	Sequence 76, Appl	c2569	13.6	0.2	20	1	US-09-489-866A-60	Sequence 60, Appl
2497	13.6	0.2	20	1	US-08-850-347-8	Sequence 8, Appl1	c2570	13.6	0.2	20	1	US-09-085-273-5	Sequence 5, Appl1
c2498	13.6	0.2	20	1	US-09-062-416-27	Sequence 27, Appl	c2571	13.6	0.2	20	1	US-09-428-583-70	Sequence 70, Appl
c2499	13.6	0.2	20	1	US-09-128-494-20	Sequence 20, Appl	2572	13.6	0.2	20	1	US-09-593-711A-155	Sequence 155, App
2500	13.6	0.2	20	1	US-08-990-065-8	Sequence 8, Appl1	2573	13.6	0.2	20	1	US-09-593-711A-160	Sequence 160, App
c2501	13.6	0.2	20	1	US-08-930-601-5	Sequence 5, Appl1	c2574	13.6	0.2	20	1	US-08-836-031-2	Sequence 2, Appl1
2502	13.6	0.2	20	1	US-09-074-357-9	Sequence 9, Appl1	c2575	13.6	0.2	20	1	US-09-430-033-2	Sequence 2, Appl1
c2503	13.6	0.2	20	1	US-09-280-799-52	Sequence 52, Appl	2576	13.6	0.2	20	1	US-09-244-796-31	Sequence 31, Appl1
c2504	13.6	0.2	20	1	US-09-280-799-175	Sequence 175, App	2577	13.6	0.2	20	1	US-09-322-360-4	Sequence 4, Appl1
c2505	13.6	0.2	20	1	US-09-150-805-15	Sequence 15, App	2578	13.6	0.2	20	1	US-09-484-617-93	Sequence 93, Appl
c2506	13.6	0.2	20	1	US-09-150-805-17	Sequence 17, Appl	c2579	13.6	0.2	20	1	US-09-484-617-137	Sequence 137, App
c2507	13.6	0.2	20	1	US-09-429-323-26	Sequence 26, Appl	2580	13.6	0.2	20	1	US-09-484-617-151	Sequence 151, App
c2508	13.6	0.2	20	1	US-09-429-323-30	Sequence 30, Appl	2581	13.6	0.2	20	1	US-08-890-865A-5	Sequence 5, Appl1
2509	13.6	0.2	20	1	US-09-429-323-46	Sequence 46, Appl	c2582	13.6	0.2	20	1	US-09-354-133-5	Sequence 5, Appl1
2510	13.6	0.2	20	1	US-08-765-340-19	Sequence 19, Appl	2583	13.6	0.2	20	1	US-09-290-452-5	Sequence 5, Appl1
c2511	13.6	0.2	20	1	US-08-765-340-64	Sequence 64, Appl	2584	13.6	0.2	20	1	US-09-364-416-22	Sequence 22, Appl
c2512	13.6	0.2	20	1	US-08-765-340-82	Sequence 82, Appl	2585	13.6	0.2	20	1	US-09-364-416-63	Sequence 63, Appl
2513	13.6	0.2	20	1	US-09-249-215-172	Sequence 172, App	c2586	13.6	0.2	20	1	US-09-364-416-75	Sequence 75, Appl
2514	13.6	0.2	20	1	US-09-249-215-189	Sequence 189, App	2587	13.6	0.2	20	1	US-09-101-126-10	Sequence 10, Appl
c2515	13.6	0.2	20	1	US-09-288-461-23	Sequence 23, Appl	c2588	13.6	0.2	20	1	US-09-488-856A-15	Sequence 15, Appl

2589	13.6	0.2	20	1	US-09-290-338-5	Sequence 5, Appl1	2662	13.6	0.2	20	1	US-09-238-710-11	Sequence 31, Appl1
2590	13.6	0.2	20	1	US-09-290-338-22	Sequence 22, Appl1	2663	13.6	0.2	20	1	US-09-358-383C-21	Sequence 21, Appl1
2591	13.6	0.2	20	1	US-09-082-649B-77	Sequence 77, Appl1	2664	13.6	0.2	20	1	US-09-290-000-5	Sequence 5, Appl1
2592	13.6	0.2	20	1	US-09-082-649B-77	Sequence 77, Appl1	2665	13.6	0.2	20	1	US-09-290-000-5	Sequence 22, Appl1
2593	13.6	0.2	20	1	US-09-488-074-3	Sequence 3, Appl1	2666	13.6	0.2	20	1	US-09-389-283-17	Sequence 17, Appl1
2594	13.6	0.2	20	1	US-09-131-831B-4	Sequence 4, Appl1	2667	13.6	0.2	20	1	US-09-972-800A-45	Sequence 45, Appl1
2595	13.6	0.2	20	1	US-09-378-842-29	Sequence 29, Appl1	2668	13.6	0.2	20	1	US-09-535-170-5	Sequence 5, Appl1
2596	13.6	0.2	20	1	US-09-482-971-12	Sequence 12, Appl1	2669	13.6	0.2	20	1	US-09-422-978-4925	Sequence 4925, Ap
2597	13.6	0.2	20	1	US-09-248-386-20	Sequence 20, Appl1	2670	13.6	0.2	20	1	US-09-422-978-1168	Sequence 5168, Ap
2598	13.6	0.2	20	1	US-09-561-497-20	Sequence 20, Appl1	2671	13.6	0.2	20	1	US-09-422-978-5234	Sequence 5234, Ap
2599	13.6	0.2	20	1	US-09-561-497-42	Sequence 42, Appl1	2672	13.6	0.2	20	1	US-09-422-978-6127	Sequence 6127, Ap
2600	13.6	0.2	20	1	US-09-733-159A-29	Sequence 29, Appl1	2673	13.6	0.2	20	1	US-09-422-978-6243	Sequence 6243, Ap
2601	13.6	0.2	20	1	US-09-177-437-6	Sequence 6, Appl1	2674	13.6	0.2	20	1	US-09-422-978-8329	Sequence 8329, Ap
2602	13.6	0.2	20	1	US-09-702-246-73	Sequence 73, Appl1	2675	13.6	0.2	20	1	US-09-422-978-8529	Sequence 8529, Ap
2603	13.6	0.2	20	1	US-09-588-950A-6	Sequence 6, Appl1	2676	13.6	0.2	20	1	US-09-422-978-9857	Sequence 9857, Ap
2604	13.6	0.2	20	1	US-09-135-202-17	Sequence 17, Appl1	2677	13.6	0.2	20	1	US-09-422-978-10500	Sequence 10500, A
2605	13.6	0.2	20	1	US-09-844-634-54	Sequence 54, Appl1	2678	13.6	0.2	20	1	US-09-422-978-10511	Sequence 10511, A
2606	13.6	0.2	20	1	US-09-844-634-96	Sequence 96, Appl1	2679	13.6	0.2	20	1	US-09-422-978-11657	Sequence 11697, A
2607	13.6	0.2	20	1	US-09-844-634-159	Sequence 159, App	2680	13.6	0.2	20	1	US-08-894-454-72	Sequence 72, Appl1
2608	13.6	0.2	20	1	US-09-506-073-46	Sequence 46, Appl1	2681	13.6	0.2	20	1	US-09-060-299-240	Sequence 240, App
2609	13.6	0.2	20	1	US-09-506-073-61	Sequence 61, Appl1	2682	13.6	0.2	20	1	US-09-705-267A-57	Sequence 57, Appl1
2610	13.6	0.2	20	1	US-09-506-073-71	Sequence 71, Appl1	2683	13.6	0.2	20	1	US-09-705-267A-113	Sequence 113, App
2611	13.6	0.2	20	1	US-09-817-856-9	Sequence 9, Appl1	2684	13.6	0.2	20	1	US-09-402-923A-240	Sequence 240, App
2612	13.6	0.2	20	1	US-09-370-398-13	Sequence 13, Appl1	2685	13.6	0.2	20	1	US-09-198-452A-1563	Sequence 1563, Ap
2613	13.6	0.2	20	1	US-09-657-452A-53	Sequence 53, Appl1	2686	13.6	0.2	20	1	US-09-198-452A-1681	Sequence 1681, Ap
2614	13.6	0.2	20	1	US-09-487-792-42	Sequence 42, Appl1	2687	13.6	0.2	20	1	US-09-198-452A-1880	Sequence 1880, Ap
2615	13.6	0.2	20	1	US-09-661-753-37	Sequence 37, Appl1	2688	13.6	0.2	20	1	US-09-198-452A-2085	Sequence 2085, Ap
2616	13.6	0.2	20	1	US-09-780-175-37	Sequence 37, Appl1	2689	13.6	0.2	20	1	US-09-198-452A-2147	Sequence 2147, Ap
2617	13.6	0.2	20	1	US-09-780-175-66	Sequence 66, Appl1	2690	13.6	0.2	20	1	US-09-198-452A-2339	Sequence 2339, Ap
2618	13.6	0.2	20	1	US-09-907-843-35	Sequence 35, Appl1	2691	13.6	0.2	20	1	US-09-198-452A-2492	Sequence 2492, Ap
2619	13.6	0.2	20	1	US-09-907-843-70	Sequence 70, Appl1	2692	13.6	0.2	20	1	US-09-198-452A-2493	Sequence 2493, Ap
2620	13.6	0.2	20	1	US-09-470-443-90	Sequence 90, Appl1	2693	13.6	0.2	20	1	US-09-198-452A-2593	Sequence 2593, Ap
2621	13.6	0.2	20	1	US-09-791-211-75	Sequence 75, Appl1	2694	13.6	0.2	20	1	US-09-198-452A-3426	Sequence 3426, Ap
2622	13.6	0.2	20	1	US-09-851-062-82	Sequence 82, Appl1	2695	13.6	0.2	20	1	US-09-198-452A-3526	Sequence 3526, Ap
2623	13.6	0.2	20	1	US-09-517-467B-57	Sequence 57, Appl1	2696	13.6	0.2	20	1	US-09-198-452A-4058	Sequence 4058, Ap
2624	13.6	0.2	20	1	US-09-517-467B-125	Sequence 125, App	2697	13.6	0.2	20	1	US-09-198-452A-4567	Sequence 4527, Ap
2625	13.6	0.2	20	1	US-09-517-467B-274	Sequence 274, App	2698	13.6	0.2	20	1	US-09-198-452A-4565	Sequence 4555, Ap
2626	13.6	0.2	20	1	US-08-275-951-27	Sequence 27, Appl1	2699	13.6	0.2	20	1	US-09-198-452A-4703	Sequence 4703, Ap
2627	13.6	0.2	20	1	US-08-275-951-28	Sequence 28, Appl1	2700	13.6	0.2	20	1	US-09-198-452A-4705	Sequence 4705, Ap
2628	13.6	0.2	20	1	US-08-275-951-29	Sequence 29, Appl1	2701	13.6	0.2	20	1	US-09-198-452A-4710	Sequence 4710, Ap
2629	13.6	0.2	20	1	US-08-275-951-30	Sequence 30, Appl1	2702	13.6	0.2	20	1	US-09-198-452A-4715	Sequence 4715, Ap
2630	13.6	0.2	20	1	US-08-275-951-63	Sequence 63, Appl1	2703	13.6	0.2	20	1	US-09-198-452A-4808	Sequence 4808, Ap
2631	13.6	0.2	20	1	US-08-802-331-32	Sequence 32, Appl1	2704	13.6	0.2	20	1	US-09-198-452A-5008	Sequence 5028, Ap
2632	13.6	0.2	20	1	US-09-920-672-33	Sequence 33, Appl1	2705	13.6	0.2	20	1	US-09-198-452A-5038	Sequence 5038, Ap
2633	13.6	0.2	20	1	US-09-920-672-51	Sequence 51, Appl1	2706	13.6	0.2	20	1	US-09-198-452A-5266	Sequence 5266, Ap
2634	13.6	0.2	20	1	US-08-626-285-26	Sequence 26, Appl1	2707	13.6	0.2	20	1	US-09-198-452A-5520	Sequence 5520, Ap
2635	13.6	0.2	20	1	US-09-679-185-6	Sequence 6, Appl1	2708	13.6	0.2	20	1	US-09-198-452A-5527	Sequence 5527, Ap
2636	13.6	0.2	20	1	US-09-531-000-64	Sequence 64, Appl1	2709	13.6	0.2	20	1	US-09-198-452A-5565	Sequence 5565, Ap
2637	13.6	0.2	20	1	US-09-531-000-64	Sequence 64, Appl1	2710	13.6	0.2	20	1	US-09-198-452A-5565	Sequence 5565, Ap
2638	13.6	0.2	20	1	US-09-780-049-86	Sequence 86, Appl1	2711	13.6	0.2	20	1	US-09-198-452A-5857	Sequence 5857, Ap
2639	13.6	0.2	20	1	US-09-291-129-2	Sequence 2, Appl1	2712	13.6	0.2	20	1	US-09-198-452A-6061	Sequence 6061, Ap
2640	13.6	0.2	20	1	US-09-291-129-13	Sequence 13, Appl1	2713	13.6	0.2	20	1	US-09-198-452A-6061	Sequence 6061, Ap
2641	13.6	0.2	20	1	US-09-475-947A-56	Sequence 56, Appl1	2714	13.6	0.2	20	1	US-09-198-452A-6585	Sequence 6585, Ap
2642	13.6	0.2	20	1	US-09-908-594-42	Sequence 42, Appl1	2715	13.6	0.2	20	1	US-09-198-452A-6585	Sequence 6585, Ap
2643	13.6	0.2	20	1	US-09-706-197-84	Sequence 84, Appl1	2716	13.6	0.2	20	1	US-09-582-337-3	Sequence 6752, Ap
2644	13.6	0.2	20	1	US-09-698-505A-36	Sequence 36, Appl1	2717	13.6	0.2	20	1	US-09-509-595-62	Sequence 3, Appl1
2645	13.6	0.2	20	1	US-09-920-668-52	Sequence 32, Appl1	2718	13.6	0.2	20	1	US-09-594-594A-5	Sequence 67, Appl1
2646	13.6	0.2	20	1	US-10-090-190-13	Sequence 13, Appl1	2719	13.6	0.2	20	1	US-09-623-634A-10	Sequence 10, Appl1
2647	13.6	0.2	20	1	US-09-213-383-39	Sequence 29, Appl1	2720	13.6	0.2	20	1	US-09-623-634A-11	Sequence 11, Appl1
2648	13.6	0.2	20	1	US-09-213-383-37	Sequence 37, Appl1	2721	13.6	0.2	20	1	US-09-823-634A-12	Sequence 12, Appl1
2649	13.6	0.2	20	1	US-09-213-383-45	Sequence 45, Appl1	2722	13.6	0.2	20	1	US-09-823-634A-13	Sequence 13, Appl1
2650	13.6	0.2	20	1	US-09-213-383-65	Sequence 65, Appl1	2723	13.6	0.2	20	1	US-09-823-634A-14	Sequence 14, Appl1
2651	13.6	0.2	20	1	US-09-844-521-67	Sequence 67, Appl1	2724	13.6	0.2	20	1	US-09-823-634A-15	Sequence 15, Appl1
2652	13.6	0.2	20	1	US-09-629-644A-131	Sequence 131, App	2725	13.6	0.2	20	1	US-09-823-634A-16	Sequence 16, Appl1
2653	13.6	0.2	20	1	US-09-629-644A-131	Sequence 131, App	2726	13.6	0.2	20	1	US-09-823-634A-17	Sequence 17, Appl1
2654	13.6	0.2	20	1	US-08-545-573A-31	Sequence 31, Appl1	2727	13.6	0.2	20	1	US-09-823-634A-18	Sequence 18, Appl1
2655	13.6	0.2	20	1	US-08-569-284-26	Sequence 26, Appl1	2728	13.6	0.2	20	1	US-09-823-634A-19	Sequence 19, Appl1
2656	13.6	0.2	20	1	US-09-898-361-87	Sequence 87, Appl1	2729	13.6	0.2	20	1	US-09-823-634A-15	Sequence 15, Appl1
2657	13.6	0.2	20	1	US-09-898-361-151	Sequence 151, App	2730	13.6	0.2	20	1	US-09-823-634A-16	Sequence 16, Appl1
2658	13.6	0.2	20	1	US-09-657-346A-59	Sequence 59, Appl1	2731	13.6	0.2	20	1	US-09-823-634A-17	Sequence 17, Appl1
2659	13.6	0.2	20	1	US-09-657-346A-70	Sequence 70, Appl1	2732	13.6	0.2	20	1	US-09-823-647B-8	Sequence 8, Appl1
2660	13.6	0.2	20	1	US-09-668-313A-43	Sequence 43, Appl1	2733	13.6	0.2	20	1	US-09-823-647B-9	Sequence 9, Appl1
2661	13.6	0.2	20	1	US-09-668-313A-75	Sequence 75, Appl1	2734	13.6	0.2	20	1	US-09-823-647B-10	Sequence 10, Appl1

2735	13.6	0.2	20	1	US-09-823-647B-11	Sequence 11, Appl	2808	13.4	0.2	15	1	US-08-832-021-38	Sequence 38, Appl
2736	13.6	0.2	20	1	US-09-823-647B-12	Sequence 12, Appl	2809	13.4	0.2	15	1	US-08-832-021-44	Sequence 44, Appl
2737	13.6	0.2	20	1	US-09-823-647B-13	Sequence 13, Appl	2810	13.4	0.2	15	1	US-08-832-021-48	Sequence 48, Appl
2738	13.6	0.2	20	1	US-09-823-647B-14	Sequence 14, Appl	2811	13.4	0.2	15	1	US-08-832-021-50	Sequence 50, Appl
2739	13.6	0.2	20	1	US-09-823-647B-15	Sequence 15, Appl	2812	13.4	0.2	15	1	US-08-832-021-52	Sequence 52, Appl
2740	13.6	0.2	20	1	US-09-823-647B-16	Sequence 16, Appl	2813	13.4	0.2	15	1	US-08-832-021-54	Sequence 54, Appl
2741	13.6	0.2	20	1	US-09-823-647B-17	Sequence 17, Appl	2814	13.4	0.2	15	1	US-08-832-021-55	Sequence 55, Appl
2742	13.6	0.2	20	1	US-09-825-497A-22	Sequence 29, Appl	2815	13.4	0.2	15	1	US-08-832-021-56	Sequence 56, Appl
2743	13.6	0.2	20	1	US-10-072-094-79	Sequence 72, Appl	2816	13.4	0.2	15	1	US-08-832-021-58	Sequence 58, Appl
2744	13.6	0.2	20	1	US-09-780-045-24	Sequence 10, Appl	2817	13.4	0.2	15	1	US-08-832-021-59	Sequence 59, Appl
2745	13.6	0.2	20	1	US-09-689-065B-10	Sequence 24, Appl	2818	13.4	0.2	15	1	US-08-832-021-60	Sequence 60, Appl
2746	13.6	0.2	20	1	US-08-944-410-7	Sequence 79, Appl	2819	13.4	0.2	15	1	US-08-913-843-25	Sequence 25, Appl
2747	13.6	0.2	20	1	US-09-526-193A-79	Sequence 16, Appl	2820	13.4	0.2	15	1	US-09-071-885-359	Sequence 359, App
2748	13.6	0.2	20	1	US-09-434-840-16	Sequence 8, Appl	2821	13.4	0.2	15	1	US-09-180-437-104	Sequence 104, App
2749	13.6	0.2	20	1	US-09-754-311B-8	Sequence 5, Appl	2822	13.4	0.2	15	1	US-09-054-837-28	Sequence 28, Appl
2750	13.6	0.2	20	1	US-09-916-963-5	Sequence 8, Appl	2823	13.4	0.2	15	1	US-09-580-799C-35	Sequence 25, Appl
2751	13.6	0.2	20	1	US-09-664-846A-2	Sequence 161, App	2824	13.4	0.2	15	1	US-09-081-646-207	Sequence 207, App
2752	13.6	0.2	20	1	US-09-660-473-161	Sequence 3, Appl	2825	13.4	0.2	15	1	US-09-081-646-788	Sequence 788, App
2753	13.6	0.2	20	1	US-09-092-218-3	Sequence 93, Appl	2826	13.4	0.2	15	1	US-09-018-834C-6	Sequence 6, Appl
2754	13.6	0.2	20	1	US-09-980-052-93	Sequence 7, Appl	2827	13.4	0.2	15	1	US-09-031-952-7	Sequence 7, Appl
2755	13.6	0.2	20	1	US-09-495-714C-7	Sequence 9, Appl	2828	13.4	0.2	15	1	US-09-475-947A-164	Sequence 164, App
2756	13.6	0.2	20	1	PCT-US91-05742-9	Sequence 11, Appl	2829	13.4	0.2	15	1	US-09-640-953-28	Sequence 28, Appl
2757	13.6	0.2	20	1	PCT-US91-05742-11	Sequence 23, Appl	2830	13.4	0.2	15	1	US-09-491-358C-19	Sequence 19, Appl
2758	13.6	0.2	20	1	PCT-US93-04863-23	Sequence 60, Appl	2831	13.4	0.2	15	1	PCT-US91-01574-20	Sequence 20, Appl
2759	13.6	0.2	20	1	PCT-US95-04477-60	Sequence 36, Appl	2832	13.4	0.2	16	1	US-08-753-147-188	Sequence 188, App
2760	13.6	0.2	20	1	PCT-US95-06379-36	Sequence 44, Appl	2833	13.4	0.2	16	1	US-08-173-489C-126	Sequence 126, App
2761	13.6	0.2	20	1	PCT-US95-07111A-44	Sequence 55, Appl	2834	13.4	0.2	16	1	US-08-770-238A-62	Sequence 62, Appl
2762	13.6	0.2	20	1	PCT-US95-07744A-55	Sequence 40, Appl	2835	13.4	0.2	16	1	US-08-454-099-8	Sequence 8, Appl
2763	13.6	0.2	20	1	PCT-US95-14148-40	Sequence 40, Appl	2836	13.4	0.2	16	1	US-08-645-411C-1	Sequence 1, Appl
2764	13.6	0.2	20	1	PCT-US95-15327-48	Sequence 10, Appl	2837	13.4	0.2	16	1	US-08-645-411C-2	Sequence 2, Appl
2765	13.6	0.2	20	1	PCT-US96-00331-10	Sequence 5, Appl	2838	13.4	0.2	16	1	US-08-645-411C-6	Sequence 6, Appl
2766	13.6	0.2	21	1	US-08-935-896-13	Sequence 13, Appl	2839	13.4	0.2	16	1	US-08-645-411C-7	Sequence 7, Appl
2767	13.6	0.2	21	1	US-08-933-149-13	Sequence 13, Appl	2840	13.4	0.2	16	1	US-08-645-411C-8	Sequence 8, Appl
2768	13.6	0.2	21	1	US-09-082-343-13	Sequence 10, Appl	2841	13.4	0.2	16	1	US-08-645-411C-9	Sequence 9, Appl
2769	13.6	0.2	21	1	US-08-863-639A-10	Sequence 13, Appl	2842	13.4	0.2	16	1	US-09-371-772B-5982	Sequence 5982, Ap
2770	13.6	0.2	21	1	US-08-863-639A-13	Sequence 13, Appl	2843	13.4	0.2	16	1	US-09-479-005A-95	Sequence 95, Appl
2771	13.6	0.2	21	1	US-08-863-639A-13	Sequence 13, Appl	2844	13.4	0.2	16	1	US-09-479-005A-987	Sequence 487, App
2772	13.6	0.2	21	1	US-08-416-214A-12	Sequence 12, Appl	2845	13.4	0.2	16	1	PCT-US96-01600-8	Sequence 8, Appl
2773	13.6	0.2	21	1	US-09-082-353-13	Sequence 13, Appl	2846	13.4	0.2	17	1	US-08-045-264A-3	Sequence 3, Appl
2774	13.6	0.2	21	1	US-09-162-622-13	Sequence 13, Appl	2847	13.4	0.2	17	1	US-08-281-940-24	Sequence 24, Appl
2775	13.6	0.2	21	1	PCT-US96-08235-13	Sequence 13, Appl	2848	13.4	0.2	17	1	US-08-373-124A-316	Sequence 316, App
2776	13.6	0.2	21	1	US-09-509-015-13	Sequence 46, Appl	2849	13.4	0.2	17	1	US-08-373-124A-530	Sequence 530, App
2777	13.6	0.2	21	1	US-09-164-349B-6	Sequence 6, Appl	2850	13.4	0.2	17	1	US-08-373-124A-1969	Sequence 1969, Ap
2778	13.6	0.2	24	1	US-09-721-154-2	Sequence 11, Appl	2851	13.4	0.2	17	1	US-08-373-124A-1974	Sequence 1974, App
2779	13.6	0.2	24	1	US-08-014-943A-11	Sequence 46, Appl	2852	13.4	0.2	17	1	US-08-373-124A-2051	Sequence 2051, Ap
2780	13.6	0.2	24	1	US-08-486-421-46	Sequence 46, Appl	2853	13.4	0.2	17	1	US-08-373-124A-2055	Sequence 2055, Ap
2781	13.6	0.2	24	1	US-08-486-809-46	Sequence 85, Appl	2854	13.4	0.2	17	1	US-08-373-124A-2141	Sequence 2141, Ap
2782	13.6	0.2	24	1	US-08-486-809-46	Sequence 85, Appl	2855	13.4	0.2	17	1	US-08-482-115B-30	Sequence 30, Appl
2783	13.6	0.2	30	1	US-08-449-315-85	Sequence 85, Appl	2856	13.4	0.2	17	1	US-08-327-526A-28	Sequence 28, Appl
2784	13.6	0.2	30	1	US-08-449-315-85	Sequence 85, Appl	2857	13.4	0.2	17	1	US-08-435-628-2051	Sequence 2051, Ap
2785	13.6	0.2	30	1	US-08-449-315-85	Sequence 85, Appl	2858	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
2786	13.6	0.2	30	1	US-08-449-315-85	Sequence 85, Appl	2859	13.4	0.2	17	1	US-08-435-628-2141	Sequence 2141, Ap
2787	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2860	13.4	0.2	17	1	US-08-435-628-2151	Sequence 2151, Ap
2788	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2861	13.4	0.2	17	1	US-08-435-628-2151	Sequence 2151, Ap
2789	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2862	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2790	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2863	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2791	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2864	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2792	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2865	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2793	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2866	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2794	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2867	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2795	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2868	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2796	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2869	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2797	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2870	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2798	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2871	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2799	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2872	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2800	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2873	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2801	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2874	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2802	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2875	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2803	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2876	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2804	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2877	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2805	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2878	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2806	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2879	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2807	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2880	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap

C2881	13.4	0.2	17	1	US-09-158-765-28	Sequence 28, Appl	2954	13.4	0.2	18	1	US-09-054-930-18	Sequence 18, Appl
2882	13.4	0.2	17	1	US-08-584-040-2187	Sequence 2187, Ap	2955	13.4	0.2	18	1	US-09-487-444-36	Sequence 36, Appl
2883	13.4	0.2	17	1	US-08-584-040-2188	Sequence 2188, Ap	2956	13.4	0.2	18	1	US-09-474-922A-57	Sequence 57, Appl
2884	13.4	0.2	17	1	US-08-584-040-2189	Sequence 2189, Ap	2957	13.4	0.2	18	1	US-09-034-205-64	Sequence 64, Appl
2885	13.4	0.2	17	1	US-08-584-040-2193	Sequence 2739, Ap	C2958	13.4	0.2	18	1	US-09-050-159-1	Sequence 1, Appl
2886	13.4	0.2	17	1	US-08-584-040-2807	Sequence 2807, Ap	C2959	13.4	0.2	18	1	US-09-269-345-1	Sequence 1, Appl
C2887	13.4	0.2	17	1	US-08-584-040-5682	Sequence 5682, Ap	C2960	13.4	0.2	18	1	US-09-313-932-169	Sequence 169, App
C2888	13.4	0.2	17	1	US-09-474-432B-896	Sequence 896, App	C2961	13.4	0.2	18	1	US-09-313-932-170	Sequence 170, App
C2889	13.4	0.2	17	1	US-09-057-351-33	Sequence 33, Appl	C2962	13.4	0.2	18	1	US-09-313-932-171	Sequence 171, App
2890	13.4	0.2	17	1	US-09-371-772B-732	Sequence 732, App	C2963	13.4	0.2	18	1	US-09-313-932-172	Sequence 172, App
2891	13.4	0.2	17	1	US-09-371-772B-733	Sequence 733, App	C2964	13.4	0.2	18	1	US-09-313-932-173	Sequence 64, Appl
2892	13.4	0.2	17	1	US-09-371-772B-734	Sequence 734, App	C2965	13.4	0.2	18	1	US-09-677-218B-64	Sequence 64, Appl
2893	13.4	0.2	17	1	US-09-371-772B-1263	Sequence 1263, Ap	2966	13.4	0.2	18	1	US-09-677-192-64	Sequence 18, Appl
2894	13.4	0.2	17	1	US-09-371-772B-1321	Sequence 1321, Ap	2967	13.4	0.2	18	1	US-09-319-588C-51	Sequence 51, Appl
C2895	13.4	0.2	17	1	US-09-371-772B-2568	Sequence 2568, Ap	2968	13.4	0.2	18	1	US-09-319-588C-80	Sequence 80, Appl
2896	13.4	0.2	17	1	US-09-371-772B-4186	Sequence 4186, Ap	2969	13.4	0.2	18	1	US-09-216-93B-314	Sequence 314, App
2897	13.4	0.2	17	1	US-09-371-772B-5287	Sequence 5287, Ap	2970	13.4	0.2	18	1	US-09-197-224-13	Sequence 13, Appl
2898	13.4	0.2	17	1	US-09-371-772B-5594	Sequence 5594, Ap	2971	13.4	0.2	18	1	US-09-422-978-6008	Sequence 6008, Ap
C2899	13.4	0.2	17	1	US-09-796-071-38	Sequence 28, Appl	C2972	13.4	0.2	18	1	US-09-422-978-7515	Sequence 7515, Ap
C2900	13.4	0.2	17	1	US-09-476-387-895	Sequence 895, App	C2973	13.4	0.2	18	1	US-09-422-978-7519	Sequence 7519, Ap
2901	13.4	0.2	17	1	US-09-401-063-116	Sequence 116, App	2974	13.4	0.2	18	1	US-09-422-978-8959	Sequence 8959, Ap
2902	13.4	0.2	17	1	US-09-401-063-517	Sequence 617, App	C2975	13.4	0.2	18	1	US-09-422-978-9179	Sequence 9179, App
2903	13.4	0.2	17	1	US-09-827-998-102	Sequence 102, App	C2976	13.4	0.2	18	1	US-09-422-978-11146	Sequence 11146, A
2904	13.4	0.2	17	1	US-09-827-998-103	Sequence 103, App	2977	13.4	0.2	18	1	US-09-230-652-67	Sequence 67, Appl
2905	13.4	0.2	17	1	US-09-827-998-104	Sequence 104, App	2978	13.4	0.2	18	1	US-09-197-321-13	Sequence 13, Appl
2906	13.4	0.2	17	1	US-09-827-998-371	Sequence 371, App	2979	13.4	0.2	18	1	US-09-572-392A-13	Sequence 13, Appl
2907	13.4	0.2	17	1	US-09-827-998-372	Sequence 372, App	2980	13.4	0.2	18	1	US-09-723-756-13	Sequence 13, Appl
2908	13.4	0.2	17	1	US-09-827-998-373	Sequence 373, App	2981	13.4	0.2	18	1	US-09-532-940-13	Sequence 13, Appl
2909	13.4	0.2	17	1	US-09-866-108A-551	Sequence 551, App	2982	13.4	0.2	18	1	US-09-710-693-13	Sequence 13, Appl
2910	13.4	0.2	17	1	US-09-866-108A-552	Sequence 552, App	C2983	13.4	0.2	18	1	PCT-US91-03056-7	Sequence 7, Appl
C2911	13.4	0.2	17	1	US-09-866-108A-2191	Sequence 2191, Ap	C2984	13.4	0.2	18	1	US-08-127-854-47	Sequence 47, Appl
C2912	13.4	0.2	17	1	US-09-866-108A-2194	Sequence 2194, Ap	C2985	13.4	0.2	19	1	US-08-255-892-66	Sequence 66, Appl
C2913	13.4	0.2	17	1	US-09-866-108A-2667	Sequence 2667, Ap	2986	13.4	0.2	19	1	US-08-257-073-106	Sequence 106, App
C2914	13.4	0.2	17	1	US-09-866-108A-5949	Sequence 5949, Ap	C2987	13.4	0.2	19	1	US-08-184-009-124	Sequence 124, App
C2915	13.4	0.2	17	1	US-09-866-108A-5950	Sequence 5950, Ap	C2988	13.4	0.2	19	1	US-08-389-360-7	Sequence 7, Appl
2916	13.4	0.2	17	1	US-09-866-108A-6257	Sequence 6257, Ap	2989	13.4	0.2	19	1	US-08-458-356-124	Sequence 124, App
2917	13.4	0.2	17	1	US-09-866-108A-6258	Sequence 6258, Ap	C2990	13.4	0.2	19	1	US-09-038-328-7	Sequence 7, Appl
2918	13.4	0.2	17	1	US-09-866-108A-6259	Sequence 6259, Ap	2991	13.4	0.2	19	1	US-09-092-077-15	Sequence 15, Appl
C2919	13.4	0.2	17	1	US-09-866-108A-7070	Sequence 7070, Ap	2992	13.4	0.2	19	1	US-09-183-931-16	Sequence 16, Appl
2920	13.4	0.2	17	1	US-09-866-108A-7588	Sequence 7588, Ap	C2993	13.4	0.2	19	1	US-08-460-736-124	Sequence 124, App
2921	13.4	0.2	17	1	US-09-866-108A-7589	Sequence 7589, Ap	C2994	13.4	0.2	19	1	US-09-338-907-464	Sequence 464, App
C2922	13.4	0.2	17	1	US-09-866-108A-7583	Sequence 7583, Ap	C2995	13.4	0.2	19	1	US-09-345-882-106	Sequence 106, App
C2923	13.4	0.2	17	1	US-09-866-108A-8872	Sequence 8872, Ap	C2996	13.4	0.2	19	1	US-09-345-882-106	Sequence 106, App
C2924	13.4	0.2	17	1	US-09-866-108A-8873	Sequence 8873, Ap	2997	13.4	0.2	19	1	US-09-345-882-106	Sequence 106, App
C2925	13.4	0.2	17	1	US-09-866-108A-8874	Sequence 8874, Ap	C2998	13.4	0.2	19	1	US-09-345-882-106	Sequence 106, App
2926	13.4	0.2	17	1	US-09-866-108A-9377	Sequence 9377, Ap	2999	13.4	0.2	19	1	US-09-652-402A-34	Sequence 34, Appl
2927	13.4	0.2	17	1	US-09-866-108A-9378	Sequence 9378, Ap	3000	13.4	0.2	19	1	US-09-652-402A-34	Sequence 34, Appl
2928	13.4	0.2	17	1	US-09-866-108A-9379	Sequence 9379, Ap	C3001	13.4	0.2	19	1	US-09-435-524-7	Sequence 7, Appl
2929	13.4	0.2	17	1	PCT-US91-01574-7	Sequence 7, Appl	3002	13.4	0.2	19	1	US-09-435-524-7	Sequence 7, Appl
2930	13.4	0.2	17	1	PCT-US91-03680-7	Sequence 7, Appl	C3003	13.4	0.2	19	1	US-09-422-978-4166	Sequence 4166, Ap
C2931	13.4	0.2	18	1	US-07-766-751-2	Sequence 2, Appl	3004	13.4	0.2	19	1	US-09-422-978-4463	Sequence 4463, Ap
2932	13.4	0.2	18	1	US-08-170-095B-31	Sequence 31, Appl	3005	13.4	0.2	19	1	US-09-422-978-4463	Sequence 4463, Ap
C2933	13.4	0.2	18	1	US-08-170-095B-34	Sequence 34, Appl	3006	13.4	0.2	19	1	US-09-422-978-4923	Sequence 4923, Ap
2934	13.4	0.2	18	1	US-08-216-276A-7	Sequence 7, Appl	3007	13.4	0.2	19	1	US-09-422-978-5928	Sequence 5928, Ap
C2935	13.4	0.2	18	1	US-08-216-276A-10	Sequence 10, Appl	3008	13.4	0.2	19	1	US-09-422-978-6997	Sequence 6997, Ap
C2936	13.4	0.2	18	1	US-08-330-850-1122	Sequence 1122, Ap	3009	13.4	0.2	19	1	US-09-422-978-8611	Sequence 8611, Ap
2937	13.4	0.2	18	1	US-08-336-866-91	Sequence 31, Appl	C3010	13.4	0.2	19	1	US-09-422-978-8930	Sequence 8930, Ap
C2938	13.4	0.2	18	1	US-08-336-866-94	Sequence 34, Appl	3011	13.4	0.2	19	1	US-09-422-978-9853	Sequence 9853, Ap
2939	13.4	0.2	18	1	US-08-363-240A-1112	Sequence 1112, Ap	3012	13.4	0.2	19	1	US-09-422-978-10908	Sequence 10908, A
C2940	13.4	0.2	18	1	US-08-363-240A-1223	Sequence 1223, Ap	3013	13.4	0.2	19	1	US-09-747-391-164	Sequence 7, Appl
C2941	13.4	0.2	18	1	US-08-435-634-1122	Sequence 1122, Ap	C3014	13.4	0.2	19	1	PCT-US91-03680-2	Sequence 2, Appl
2942	13.4	0.2	18	1	US-08-627-254C-21	Sequence 21, Appl	C3015	13.4	0.2	19	1	PCT-US91-03680-9	Sequence 9, Appl
2943	13.4	0.2	18	1	US-08-244-577-13	Sequence 13, Appl	C3016	13.4	0.2	20	1	US-08-487-141B-19	Sequence 19, Appl
2944	13.4	0.2	18	1	US-09-212-771-28	Sequence 28, Appl	C3017	13.4	0.2	20	1	US-08-927-561-19	Sequence 19, Appl
2945	13.4	0.2	18	1	US-09-205-860-75	Sequence 75, Appl	C3018	13.4	0.2	20	1	PCT-US96-09388-19	Sequence 19, Appl
2946	13.4	0.2	18	1	US-09-200-141-18	Sequence 18, Appl	C3019	13.4	0.2	20	1	US-08-375-951-46	Sequence 46, Appl
C2947	13.4	0.2	18	1	US-09-106-038A-45	Sequence 45, Appl	C3020	13.4	0.2	20	1	US-09-358-383C-21	Sequence 21, Appl
C2948	13.4	0.2	18	1	US-09-945-654-16	Sequence 16, Appl	3021	13.4	0.2	20	1	US-07-884-004A-9	Sequence 9, Appl
C2949	13.4	0.2	18	1	US-09-166-186-169	Sequence 169, App	3022	13.4	0.2	20	1	US-08-071-601-15	Sequence 15, Appl
C2950	13.4	0.2	18	1	US-09-166-186-170	Sequence 170, App	C3023	13.4	0.2	20	1	US-08-271-942A-116	Sequence 116, App
C2951	13.4	0.2	18	1	US-09-166-186-171	Sequence 171, App	C3024	13.4	0.2	20	1	US-07-977-284A-118	Sequence 118, App
C2952	13.4	0.2	18	1	US-09-166-186-172	Sequence 172, App	3025	13.4	0.2	20	1	US-07-977-284A-118	Sequence 118, App
C2953	13.4	0.2	18	1	US-09-289-466-84	Sequence 84, Appl	3026	13.4	0.2	20	1	US-06-250-856A-15	Sequence 15, Appl

C3027	13.4	0.2	20	1	US-08-118-441-3	Sequence 3, Appl1	C3100	13.4	0.2	20	1	US-09-021-701-665	Sequence 665, App
3028	13.4	0.2	20	1	US-08-222-177A-237	Sequence 237, App	C3101	13.4	0.2	20	1	US-09-021-701-666	Sequence 666, App
3029	13.4	0.2	20	1	US-08-222-177A-285	Sequence 285, App	3102	13.4	0.2	20	1	US-09-021-701-726	Sequence 726, App
C3030	13.4	0.2	20	1	US-08-202-990-3	Sequence 3, Appl1	C3103	13.4	0.2	20	1	US-09-021-701-1069	Sequence 1069, App
3031	13.4	0.2	20	1	US-07-976-103A-14	Sequence 14, Appl1	C3104	13.4	0.2	20	1	US-09-021-701-1070	Sequence 1070, App
C3032	13.4	0.2	20	1	US-08-458-393-9	Sequence 9, Appl1	C3105	13.4	0.2	20	1	US-09-021-701-1071	Sequence 1071, App
3033	13.4	0.2	20	1	US-08-487-141B-20	Sequence 20, Appl1	C3106	13.4	0.2	20	1	US-09-021-701-1072	Sequence 1072, App
3034	13.4	0.2	20	1	US-08-255-892-103	Sequence 103, App	C3107	13.4	0.2	20	1	US-09-021-701-1073	Sequence 1074, App
3035	13.4	0.2	20	1	US-08-171-718-13	Sequence 13, Appl1	C3108	13.4	0.2	20	1	US-09-021-701-1074	Sequence 1074, App
C3036	13.4	0.2	20	1	US-08-605-089-18	Sequence 18, Appl1	C3110	13.4	0.2	20	1	US-09-488-857B-46	Sequence 46, Appl1
C3037	13.4	0.2	20	1	US-08-665-966-16	Sequence 16, Appl1	C3111	13.4	0.2	20	1	US-09-487-368A-81	Sequence 81, Appl1
3038	13.4	0.2	20	1	US-08-473-481-1	Sequence 1, Appl1	3112	13.4	0.2	20	1	US-09-489-869-61	Sequence 62, Appl1
3039	13.4	0.2	20	1	US-08-621-100-15	Sequence 15, Appl1	3113	13.4	0.2	20	1	US-09-489-869-62	Sequence 62, Appl1
3040	13.4	0.2	20	1	US-08-117-952-142	Sequence 142, App	C3113	13.4	0.2	20	1	US-09-240-473-7	Sequence 7, Appl1
3041	13.4	0.2	20	1	US-08-117-952-148	Sequence 148, App	C3114	13.4	0.2	20	1	US-09-280-590A-5	Sequence 5, Appl1
C3042	13.4	0.2	20	1	US-08-651-692-10	Sequence 10, Appl1	C3115	13.4	0.2	20	1	US-08-957-351-17	Sequence 17, Appl1
C3043	13.4	0.2	20	1	US-08-927-561-20	Sequence 20, Appl1	C3116	13.4	0.2	20	1	US-09-015-160-50	Sequence 50, Appl1
C3044	13.4	0.2	20	1	US-08-761-243C-10	Sequence 10, Appl1	3117	13.4	0.2	20	1	US-08-984-709A-41	Sequence 41, Appl1
C3045	13.4	0.2	20	1	US-08-478-178A-115	Sequence 115, App	3118	13.4	0.2	20	1	US-09-657-042A-73	Sequence 73, Appl1
C3046	13.4	0.2	20	1	US-08-488-177-115	Sequence 115, App	C3119	13.4	0.2	20	1	US-08-829-637A-115	Sequence 115, App
C3047	13.4	0.2	20	1	US-08-481-072A-115	Sequence 115, App	C3120	13.4	0.2	20	1	US-09-232-346-56	Sequence 56, Appl1
C3048	13.4	0.2	20	1	US-08-664-336-115	Sequence 115, App	3121	13.4	0.2	20	1	US-09-629-645A-24	Sequence 24, Appl1
C3049	13.4	0.2	20	1	US-08-866-650-7	Sequence 7, Appl1	C3122	13.4	0.2	20	1	US-09-561-497-74	Sequence 74, Appl1
C3050	13.4	0.2	20	1	US-08-256-426B-116	Sequence 116, App	C3123	13.4	0.2	20	1	US-09-561-497-75	Sequence 75, Appl1
3051	13.4	0.2	20	1	US-08-975-211-27	Sequence 27, App	C3125	13.4	0.2	20	1	US-09-702-251-67	Sequence 67, Appl1
3052	13.4	0.2	20	1	US-08-756-806A-15	Sequence 15, App	C3126	13.4	0.2	20	1	US-09-173-658B-5	Sequence 5, Appl1
C3053	13.4	0.2	20	1	US-08-481-066A-115	Sequence 115, App	3127	13.4	0.2	20	1	US-08-599-738A-14	Sequence 14, Appl1
C3055	13.4	0.2	20	1	US-08-343-443B-119	Sequence 119, App	C3128	13.4	0.2	20	1	US-09-689-255C-22	Sequence 22, Appl1
C3056	13.4	0.2	20	1	US-09-021-287-7	Sequence 7, Appl1	3129	13.4	0.2	20	1	US-09-167-109-50	Sequence 50, Appl1
3057	13.4	0.2	20	1	US-08-507-032-5	Sequence 5, Appl1	C3130	13.4	0.2	20	1	US-09-798-096-49	Sequence 49, Appl1
3058	13.4	0.2	20	1	US-08-874-186-48	Sequence 48, App	C3131	13.4	0.2	20	1	US-09-844-63A-45	Sequence 45, Appl1
C3059	13.4	0.2	20	1	US-08-940-250-9	Sequence 9, Appl1	3132	13.4	0.2	20	1	US-09-506-073-15	Sequence 15, Appl1
3060	13.4	0.2	20	1	US-08-487-799-63	Sequence 63, Appl1	C3133	13.4	0.2	20	1	US-08-744-481A-52	Sequence 52, Appl1
C3061	13.4	0.2	20	1	US-08-578-615A-77	Sequence 77, App	C3135	13.4	0.2	20	1	US-09-341-444A-12	Sequence 12, Appl1
3062	13.4	0.2	20	1	US-08-755-587-172	Sequence 172, App	3136	13.4	0.2	20	1	US-09-907-843-18	Sequence 18, Appl1
C3063	13.4	0.2	20	1	US-09-357-070-8	Sequence 8, Appl1	3137	13.4	0.2	20	1	US-09-658-679A-31	Sequence 31, Appl1
3064	13.4	0.2	20	1	US-09-344-001-20	Sequence 20, App	3138	13.4	0.2	20	1	US-09-676-610B-182	Sequence 182, App
C3065	13.4	0.2	20	1	US-08-779-916A-106	Sequence 106, App	C3139	13.4	0.2	20	1	US-09-725-265-33	Sequence 33, Appl1
C3066	13.4	0.2	20	1	US-09-041-780-16	Sequence 16, App	C3140	13.4	0.2	20	1	US-09-851-063-79	Sequence 79, App
C3067	13.4	0.2	20	1	US-08-338-579A-3	Sequence 3, Appl1	C3141	13.4	0.2	20	1	US-09-517-467B-229	Sequence 229, App
3068	13.4	0.2	20	1	US-08-478-087-13	Sequence 13, Appl1	C3142	13.4	0.2	20	1	US-09-091-952A-171	Sequence 171, App
C3069	13.4	0.2	20	1	US-09-166-186-69	Sequence 69, App	C3143	13.4	0.2	20	1	US-09-690-364-97	Sequence 97, App
C3070	13.4	0.2	20	1	US-09-166-186-150	Sequence 150, App	C3144	13.4	0.2	20	1	US-09-658-679A-32	Sequence 32, Appl1
C3071	13.4	0.2	20	1	US-09-166-186-151	Sequence 151, App	C3145	13.4	0.2	20	1	US-09-725-265-33	Sequence 33, Appl1
C3072	13.4	0.2	20	1	US-09-166-186-152	Sequence 152, App	C3146	13.4	0.2	20	1	US-09-725-265-37	Sequence 37, Appl1
C3073	13.4	0.2	20	1	US-09-166-186-153	Sequence 153, App	3147	13.4	0.2	20	1	US-09-725-265-38	Sequence 38, Appl1
3074	13.4	0.2	20	1	US-09-166-186-154	Sequence 154, App	3148	13.4	0.2	20	1	US-09-659-845A-148	Sequence 148, App
3075	13.4	0.2	20	1	US-09-143-214-15	Sequence 15, App	3149	13.4	0.2	20	1	US-09-629-644A-81	Sequence 81, Appl1
C3076	13.4	0.2	20	1	US-08-850-347-10	Sequence 10, App	3150	13.4	0.2	20	1	US-09-629-644A-81	Sequence 81, Appl1
3077	13.4	0.2	20	1	US-08-903-139B-1	Sequence 1, Appl1	C3151	13.4	0.2	20	1	US-09-657-346A-125	Sequence 125, App
C3078	13.4	0.2	20	1	US-08-990-065-10	Sequence 10, App	C3152	13.4	0.2	20	1	US-09-657-346A-142	Sequence 142, App
3079	13.4	0.2	20	1	US-08-765-340-44	Sequence 44, App	3153	13.4	0.2	20	1	US-09-668-312A-143	Sequence 143, App
C3080	13.4	0.2	20	1	US-09-444-053-25	Sequence 25, App	C3154	13.4	0.2	20	1	US-09-422-978-4350	Sequence 4350, App
3081	13.4	0.2	20	1	US-09-444-053-27	Sequence 27, App	C3155	13.4	0.2	20	1	US-09-422-978-5598	Sequence 5598, App
C3082	13.4	0.2	20	1	US-08-928-941D-5	Sequence 5, Appl1	C3156	13.4	0.2	20	1	US-09-422-978-6679	Sequence 6679, App
3083	13.4	0.2	20	1	US-09-280-805-114	Sequence 114, App	3157	13.4	0.2	20	1	US-09-422-978-11055	Sequence 11055, A
C3084	13.4	0.2	20	1	US-09-101-886B-85	Sequence 85, App	C3158	13.4	0.2	20	1	US-09-422-978-11370	Sequence 11370, A
3085	13.4	0.2	20	1	US-08-908-436-8	Sequence 8, Appl1	3159	13.4	0.2	20	1	US-09-549-949B-8	Sequence 8, Appl1
C3086	13.4	0.2	20	1	US-08-836-261A-50	Sequence 50, App	3160	13.4	0.2	20	1	US-09-380-836-78	Sequence 78, App
3087	13.4	0.2	20	1	US-08-836-261A-60	Sequence 60, App	3161	13.4	0.2	20	1	US-09-705-267A-61	Sequence 61, App
C3088	13.4	0.2	20	1	US-08-193-377B-31	Sequence 31, App	C3162	13.4	0.2	20	1	US-09-705-267A-139	Sequence 139, App
C3089	13.4	0.2	20	1	US-09-193-377B-37	Sequence 37, App	C3163	13.4	0.2	20	1	US-09-198-452A-2864	Sequence 2864, App
C3090	13.4	0.2	20	1	US-09-313-932-150	Sequence 69, App	C3164	13.4	0.2	20	1	US-09-198-452A-3733	Sequence 3733, App
C3091	13.4	0.2	20	1	US-09-313-932-150	Sequence 150, App	C3165	13.4	0.2	20	1	US-09-198-452A-4959	Sequence 4959, App
C3092	13.4	0.2	20	1	US-09-313-932-152	Sequence 152, App	3167	13.4	0.2	20	1	US-09-198-452A-5083	Sequence 5083, App
C3093	13.4	0.2	20	1	US-09-313-932-153	Sequence 153, App	C3168	13.4	0.2	20	1	US-09-198-452A-5676	Sequence 5676, App
C3094	13.4	0.2	20	1	US-09-313-932-154	Sequence 154, App	C3169	13.4	0.2	20	1	US-09-198-452A-5955	Sequence 5955, App
C3095	13.4	0.2	20	1	US-09-313-932-154	Sequence 154, App	C3170	13.4	0.2	20	1	US-09-198-452A-6598	Sequence 6598, App
3097	13.4	0.2	20	1	US-08-338-352-15	Sequence 15, App	C3171	13.4	0.2	20	1	US-09-808-350-7	Sequence 7, Appl1
C3098	13.4	0.2	20	1	US-09-560-594-20	Sequence 20, App	3172	13.4	0.2	20	1	US-09-679-299A-84	Sequence 84, Appl1

C3173 13.4 0.2 20 1 US-09-679-2399A-84 Sequence 84, Appl  
C3174 13.4 0.2 20 1 US-09-081-385-112 Sequence 112, App  
3175 13.4 0.2 20 1 US-08-849-949-2 Sequence 2, Appl  
3176 13.4 0.2 20 1 US-08-849-949-10 Sequence 10, Appl  
C3177 13.4 0.2 20 1 US-08-849-949-11 Sequence 11, Appl  
3178 13.4 0.2 20 1 US-09-825-497A-27 Sequence 27, Appl  
C3179 13.4 0.2 20 1 US-09-787-375-3 Sequence 3, Appl  
3180 13.4 0.2 20 1 US-09-689-065B-20 Sequence 20, Appl  
C3181 13.4 0.2 20 1 US-09-665-615B-59 Sequence 59, Appl  
C3182 13.4 0.2 20 1 US-09-688-188B-109 Sequence 109, App  
3183 13.4 0.2 20 1 US-09-980-052-89 Sequence 89, Appl  
C3184 13.4 0.2 20 1 US-09-892-398-5 Sequence 5, Appl  
3185 13.4 0.2 20 1 US-09-730-212C-4 Sequence 4, Appl  
C3186 13.4 0.2 20 1 US-09-291-417D-109 Sequence 109, App  
C3187 13.4 0.2 20 1 PCT-US94-07770-77 Sequence 77, Appl  
C3188 13.4 0.2 20 1 PCT-US94-09851-3 Sequence 3, Appl  
C3189 13.4 0.2 20 1 PCT-US95-02311-3 Sequence 3, Appl  
3190 13.4 0.2 20 1 PCT-US95-07111A-15 Sequence 15, Appl  
C3191 13.4 0.2 20 1 PCT-US95-08604-106 Sequence 106, App  
C3192 13.4 0.2 20 1 PCT-US96-09388-20 Sequence 20, Appl  
C3193 13.4 0.2 20 1 5194596-22 Patent No. 5194596  
C3194 13.4 0.2 20 1 5219739-27 Patent No. 5219739

## ALIGNMENTS

RESULT 1  
US-08-863-639A-29/c  
; Sequence 29, Application US/08863639A  
; Patent No. 5981185  
; GENERAL INFORMATION:  
; APPLICANT: Matson, Robert S.  
; APPLICANT: Coaselin, Peter J.  
; APPLICANT: Rampal, Jang B.  
; APPLICANT: Caskey, C. T.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, 9th Floor  
; CITY: Pasadena  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Corel WordPerfect 8 version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/863,639A  
; FILING DATE: May 28, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph E. Muech  
; REGISTRATION NUMBER: 20,532  
; REFERENCE/DOCKET NUMBER: 11859-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (626) 796-4000  
; TELEFAX: (626) 795-6321  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; US-08-863-639A-29  
Query Match 0.4%; Score 27.8; DB 1; Length 33;  
Best Local Similarity 93.5%; Pred. No. 15;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7405 AGCAACATCAGCAGCAGCAGCAGCA 7435  
Db 32 AGCAGCAGCAGCAGCAGCAGCAGCA 2

RESULT 2  
US-09-306-290-25  
; Sequence 25, Application US/09306290  
; Patent No. 6221635  
; GENERAL INFORMATION:  
; APPLICANT: Rovera, Giovanni  
; APPLICANT: Rovera, Giovanni  
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE  
; FILE REFERENCE: 09924-10  
; CURRENT APPLICATION NUMBER: US/09/306,290  
; CURRENT FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer p41  
; OTHER INFORMATION: FH373  
US-09-306-290-25

Query Match 0.4%; Score 27.8; DB 1; Length 40;  
Best Local Similarity 82.1%; Pred. No. 23;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4466 TTTTCTTTTCTTTTCTTTGCTTGACATGAGGCTTGG 4504  
Db 1 TTTTCTTTTCTTTTCTTTCTATATACGAGGGTTTGG 39

RESULT 3  
US-09-475-947A-251  
; Sequence 251, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: URS00667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 251  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: human  
; US-09-475-947A-251

Query Match 0.4%; Score 26.2; DB 1; Length 33;  
Best Local Similarity 90.3%; Pred. No. 31;  
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7405 AGCAACATCAGCAGCAGCAGCAGCA 7435  
Db 2 AGCAGCAGCAGCAGCAGCAGCAGCA 32

RESULT 4  
US-08-068-747-6  
; Sequence 6, Application US/08068747  
; Patent No. 5695933  
; GENERAL INFORMATION:  
; APPLICANT: Schalling, Martin

```

; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
; US-08-068-747-6

Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 5
US-08-068-747-11/c
; Sequence 11, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
; US-08-068-747-11

Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
Db 30 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 2

RESULT 6
US-08-863-639A-30
; Sequence 30, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-30

Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```



QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435  
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

## RESULT 7

US-09-135-994-4  
Sequence 4, Application US/09135994A  
Patent No. 6280938  
GENERAL INFORMATION:  
APPLICANT: Ranum et al.  
TITLE OF INVENTION: SCAT GENE AND METHODS OF USE  
FILE REFERENCE: University of Minnesota  
CURRENT FILING DATE: 1998-08-18  
EARLIER FILING DATE: 1997-08-19  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-135-994-4

Query Match 0.3%; Score 25.8; DB 1; Length 30;  
Best Local Similarity 93.1%; Pred. No. 30;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435  
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 8  
US-09-684-843A-4  
Sequence 4, Application US/09684843A  
Patent No. 6514755  
GENERAL INFORMATION:  
APPLICANT: Ranum et al.  
TITLE OF INVENTION: SCAT GENE AND METHODS OF USE  
FILE REFERENCE: Regents of the University of Minnesota  
CURRENT FILING DATE: 2000-10-06  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,170  
PRIOR FILING DATE: 1998-08-18  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-684-843A-4

Query Match 0.3%; Score 25.8; DB 1; Length 30;  
Best Local Similarity 93.1%; Pred. No. 30;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435  
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 9  
US-08-570-155-14  
Sequence 14, Application US/08570155  
Patent No. 5962332  
GENERAL INFORMATION:  
APPLICANT: Singer, Robert H.  
APPLICANT: Taneja, Krishan L.

TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS  
NUMBER OF INVENTION: BY IN SITU HYBRIDIZATION  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,155  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/399,499  
FILING DATE: 07 March 1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/214,823  
FILING DATE: 17 March 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06353/011001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-570-155-14

Query Match 0.3%; Score 25.8; DB 1; Length 31;  
Best Local Similarity 93.1%; Pred. No. 32;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435  
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

## RESULT 10

PCT-US95-02861-14  
Sequence 14, Application PC/TUS9502861  
GENERAL INFORMATION:  
APPLICANT: Singer, Robert H.  
APPLICANT: Taneja, Krishan L.  
TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE  
TITLE OF INVENTION: REPEATS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version
SOFTWARE: #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02861
FILING DATE: 08 March 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,823
FILING DATE: 17 March 1994
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 06353/010W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-02861-14
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Query Match 0.3%; Score 25.8; DB 1; Length 31;
Best Local Similarity 93.1%; Pred. No. 32;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 7407 CAACATGAGCAGCAGCAGCAGCAGCA 7435
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29
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RESULT 11
US-08-068-747-7
Sequence 7, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-7
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Query Match 0.3%; Score 25; DB 1; Length 33;
Best Local Similarity 84.8%; Pred. No. 53;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 1 CGCGCGCGCGCGCGCGCGCGCGCGCGCG 33
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RESULT 12
US-08-863-639A-31
Sequence 31, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matsun, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Wordperfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-31
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Query Match 0.3%; Score 24.2; DB 1; Length 36;
Best Local Similarity 89.7%; Pred. No. 91;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 7406 GCAACATCAGCAGCAGCAGCAGCAGC 7434
Db 1 GCAGCAGCAGCAGCAGCAGCAGCAGCAGC 29
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RESULT 13
US-08-113-646A-42/C
Sequence 42, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
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:
: APPLICANT: PICKUP, David J.
: APPLICANT: PATEL, Dhaval Kumar
: APPLICANT: ANTCAK, James B.
: TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: NIXON & VANDERHAYE P.C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4714
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/113,646A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/084,406
: FILING DATE: 10-AUG-1987
: ATTORNEY/AGENT INFORMATION:
: NAME: WILSON, MARY J.
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 1579-20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: TELEX: 200797 NIXN UR
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA (genomic)
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: US-08-113-646A-42
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Query Match 0.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 58;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 4465 TTTTGTGCTGCTG 4489
Db 25 TTTTGTGCTGCTG 1
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RESULT 14
: US-08-465-384-4
: Sequence 4, Application US/08465384
: Patent No. 5637464
:
: GENERAL INFORMATION:
: APPLICANT: Cohen, Aharon S., Alexei
: APPLICANT: Belenky, and Maria Vilenchik
: TITLE OF INVENTION: Method of Detecting Sub-PBP Levels of
: TITLE OF INVENTION: Oligonucleotides in Biological Fluids
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Lappin & Kusner
: STREET: 200 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
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: APPLICATION NUMBER: US/08/465,384
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerner, Ann-Louise
: REGISTRATION NUMBER: 33,523
: REFERENCE/DOCKET NUMBER: HYZ-011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-330-1300
: TELEFAX: 617-330-1311
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 33 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: YES
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: US-08-465-384-4
:
Query Match 0.3%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 1,1e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 4450 TGGGTGCGATGACTTTTTTTTTTTTTTTT 4482
Db 1 TGGGTGCGAGAGTTTTTTTTTTTTTTTTTT 33
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RESULT 15
: US-08-455-627-12/C
: Sequence 12, Application US/08455627
: Patent No. 5571677
:
: GENERAL INFORMATION:
: APPLICANT: Sergei M. Gryaznov
: TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
: TITLE OF INVENTION: Connected Macromolecular Structures
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Cooley Godward LLP
: STREET: Five Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94306-2155
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,627
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Nakamura, Jackie N.
: REGISTRATION NUMBER: 35,966
: REFERENCE/DOCKET NUMBER: LYNN-003/01 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-843-5000
: TELEFAX: 415-857-0663
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
:
: US-08-455-627-12
:
Query Match 0.3%; Score 23.2; DB 1; Length 30;
Best Local Similarity 89.3%; Pred. No. 95;

```



RESULT 19  
US-09-466-138-26  
Sequence 26, Application US/09466138  
Patent No. 6153738  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, Richard  
APPLICANT: Oliveira, Baldozero M.  
TITLE OF INVENTION: Contryphan Peptides  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figs, Ernst & Kurz, P.C.  
STREET: 755 Thirteenth Street N.W., Suite 701-E  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/466,138  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/061,026  
FILING DATE:  
APPLICATION NUMBER: US 60/068,737  
FILING DATE: 24-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 2314-133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-783-6040  
TELEFAX: 202-783-6031  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-09-466-138-26  
Query Match 0.3%; Score 23.2; DB 1; Length 33;  
Best Local Similarity 89.3%; Pred. No. 1.2e+02;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4461 GACTTTTGTCTT 4488  
Db 1 GGGTTTTTTTTTTTTTTTTTTT 28  
RESULT 20  
5478746-1/c  
Patent No. 5478746  
APPLICANT: COHEN, JEFFREY I., PURCELL, ROBERT H., FEINSTONE,  
STEPHEN M., TICEHURST, JOHN R.  
TITLE OF INVENTION: CDNA ENCODING ATTENUATED CELL CULTURE  
ADAPTED HEPATITIS A VIRUS GENOME  
NUMBER OF SEQUENCES: 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/120,646  
FILING DATE: 13-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 789,640  
FILING DATE: 12-NOV-1991  
APPLICATION NUMBER: 462,916  
FILING DATE: 12-JAN-1990  
APPLICATION NUMBER: 88,220

FILING DATE: 24-AUG-1987  
APPLICATION NUMBER: 905,146  
FILING DATE: 09-SEP-1986  
APPLICATION NUMBER: 652,067  
FILING DATE: 19-SEP-1984  
APPLICATION NUMBER: 366,165  
FILING DATE: 07-APR-1982  
SEQ ID NO.1:  
LENGTH: 33  
5478746-1  
Query Match 0.3%; Score 23.2; DB 1; Length 33;  
Best Local Similarity 89.3%; Pred. No. 1.2e+02;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4463 CTTTTTTTTTTTTTTTTTTTGA 4490  
Db 29 CTTTTTTTTTTTTTTTTTTTGA 2  
RESULT 21  
US-08-863-639A-94  
Sequence 94, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel Wordperfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Muech  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-94  
Query Match 0.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7413 CAGCAGCAGCAGCAGCAGCA 7435  
Db 2 CAGCAGCAGCAGCAGCAGCA 24  
RESULT 22

```
US-08-621-914A-3
; Sequence 3, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,726
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-621-914A-3

Query Match          0.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTGTCTG 4489
DB      1 TTTTGTCTG 26

RESULT 23
US-10-003-998A-7/c
; Sequence 7, Application US/10003998A
; Patent No. 6664064
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
; FILE REFERENCE: 5438/00/EP
; CURRENT APPLICATION NUMBER: US/10/003,998A
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-998A-7

Query Match          0.3%; Score 22.8; DB 1; Length 29;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY      4464 TTTTGTCTG 4489
DB      26 TTTTGTCTG 1

RESULT 24
US-08-173-489C-20
; Sequence 20, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEBBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from n-myc
; HYPOTHETICAL: yes
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20 :FROM 1 TO 35
US-08-173-489C-20

Query Match          0.3%; Score 22.8; DB 1; Length 35;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTGTCTG 4489
DB      4 TTTTGTCTG 29

RESULT 25
US-09-244-794A-8/c
; Sequence 8, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
```

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; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-794A-8

Query Match      0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4460 GGACTTTTGTCTT 4488
Db      29 GGTGTTTTTTTTTTTTTTTTTTT 1

RESULT 26
US-09-007-005-8/c
; Sequence 8, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-8

Query Match      0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4460 GGACTTTTGTCTT 4488
Db      29 GGTGTTTTTTTTTTTTTTTTTTT 1

RESULT 27
US-09-247-190-8/c
; Sequence 8, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
```

```

; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/247,190
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-8

Query Match      0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4460 GGACTTTTGTCTT 4488
Db      29 GGTGTTTTTTTTTTTTTTTTTTT 1

RESULT 28
US-09-244-796-8/c
; Sequence 8, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-8

Query Match      0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4460 GGACTTTTGTCTT 4488
Db      29 GGTGTTTTTTTTTTTTTTTTTTT 1

RESULT 29
US-09-238-710-8/c
; Sequence 8, Application US/09238710A
; Patent No. 6518018
```

```
; GENERAL INFORMATION:
; APPLICANT: Szostek, Jack W.
; APPLICANT: Robert, Richard W.
; APPLICANT: Liu, Rihel
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350004
; CURRENT APPLICATION NUMBER: US/09/238,710A
; EARLIER FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-238-710-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4460 GGACTTTTGTCTTGTCTT 4488
Db      29 GGTTTTTTTTTTTTTTTTTTTT 1

RESULT 30
US-09-282-734-3/c
; Sequence 3, Application US/09282734A
; Patent No. 6537749
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin
US-09-282-734-3

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4460 GGACTTTTGTCTTGTCTT 4488
Db      29 GGTTTTTTTTTTTTTTTTTTTT 1

RESULT 31
US-09-750-401-10
; Sequence 10, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.

; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of GADD45
US-09-750-401-10

Query Match          0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 11.1%; Pred. No. 1.7e+02;
Matches 3; Conservative 21; Mismatches 3; Indels 0; Gaps 0;

QY      4464 TTTTGTCTTGTCTTGTCTTGA 4490
Db      5 UUUUUUUUUUUUUUUUUUUUUUUU 31

RESULT 32
US-10-003-998A-4/c
; Sequence 4, Application US/10003998A
; Patent No. 6664064
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
; FILE REFERENCE: 5438/00/EP
; CURRENT APPLICATION NUMBER: US/10/003,998A
; CURRENT FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo sapiens
US-10-003-998A-4

Query Match          0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4464 TTTTGTCTTGTCTTGTCTTGA 4490
Db      32 TTTTGTCTTGTCTTGTCTTGA 6

RESULT 33
US-09-527-345-6
; Sequence 6, Application US/09527345
; Patent No. 6331413
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/527,345
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



FEATURE:  
OTHER INFORMATION: Oligonucleotide primer ZC7231  
US-09-527-345-6

Query Match 0.3%; Score 22; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.2e+02;  
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489  
DB 1 TTTTGTCTGCTG 26

RESULT 34  
US-09-167-513-10  
Sequence 10, Application US/09167513  
Patent No. 6388064  
GENERAL INFORMATION:  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Blumberg, Hal  
TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A  
FILE REFERENCE: 97-63  
CURRENT APPLICATION NUMBER: US/09/167,513  
CURRENT FILING DATE: 1998-10-06  
EARLIER APPLICATION NUMBER: US 60/061,712  
EARLIER FILING DATE: 1997-10-06  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer ZC7231  
US-09-167-513-10

Query Match 0.3%; Score 22; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.2e+02;  
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489  
DB 1 TTTTGTCTGCTG 26

RESULT 35  
US-09-161-939A-43  
Sequence 43, Application US/09161939A  
Patent No. 6486299  
GENERAL INFORMATION:  
APPLICANT: Shimkets, Richard A.  
TITLE OF INVENTION: Genes and Proteins Predictive and Therapeutic for  
FILE REFERENCE: 15966-527  
CURRENT APPLICATION NUMBER: US/09/161,939A  
CURRENT FILING DATE: 1998-09-28  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: oligo(dT)<25>V  
US-09-161-939A-43

Query Match 0.3%; Score 22; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.2e+02;  
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489  
DB 1 TTTTGTCTGCTG 26

RESULT 36  
US-09-325-554-18  
Sequence 18, Application US/09325554  
Patent No. 6410235  
GENERAL INFORMATION:  
APPLICANT: Weindel, Kurt  
APPLICANT: Brand, Joachim  
TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX  
FILE REFERENCE: 024420-00008  
CURRENT APPLICATION NUMBER: US/09/325,554  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 198-24-900.4  
PRIOR FILING DATE: 1998-06-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent-In version 3.1  
SEQ ID NO 18  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: misc signal  
LOCATION: (27)-(27)  
OTHER INFORMATION: Y means incorporation of Amino linker-phosphoramidite subsequent  
OTHER INFORMATION: entered with 3'-O carboxymethyl digoxigenin  
US-09-325-554-18

Query Match 0.3%; Score 22; DB 1; Length 27;  
Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCT 4487  
DB 4 TTTTGTCTGCT 27

RESULT 37  
US-08-068-747-2/c  
Sequence 2, Application US/08068747  
Patent No. 5695933  
GENERAL INFORMATION:  
APPLICANT: Schalling, Martin  
APPLICANT: Hudson, Thomas J.  
APPLICANT: Housman, David E.  
TITLE OF INVENTION: Direct Determination of Expanded  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/068,747  
FILING DATE: 28-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-6141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:





TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC  
ACID MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWREY & SIMON  
STREET: 1299 PENNSYLVANIA AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14096  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: AUERBACH, JEFFREY I  
REGISTRATION NUMBER: 32,680  
REFERENCE/DOCKET NUMBER: 639-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 383-7451  
TELEFAX: (202) 383-6610  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Equus caballus  
IMMEDIATE SOURCE:  
CLONE: Biotin-T25  
PCT-US94-14096-2

Query Match 0.3%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 1.2e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4488  
Db 1 TTTTGTGCTT 25

RESULT 45  
US-08-621-914A-1  
Sequence 1, Application US/08621914A  
Patent No. 5707807  
GENERAL INFORMATION:  
APPLICANT: KATO, KIKUYA  
TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,914A

FILING DATE: 26-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LAWRENCE III, STANTON T.  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-107-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: other nucleic acid  
US-08-621-914A-1

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4488  
Db 1 TTTTGTGCTT 25

RESULT 46  
US-08-621-914A-2  
Sequence 2, Application US/08621914A  
Patent No. 5707807  
GENERAL INFORMATION:  
APPLICANT: KATO, KIKUYA  
TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,914A  
FILING DATE: 26-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LAWRENCE III, STANTON T.  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-107-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: other nucleic acid  
US-08-621-914A-2

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTT 4488  
DB 1 TTTTGTCTT 25

## RESULT 47

US-08-873-437-2  
Sequence 2, Application US/08873437  
Patent No. 6124092  
GENERAL INFORMATION:  
APPLICANT: O'Neill, Roger A.  
APPLICANT: Chen, Jer-Kang  
APPLICANT: Chiesa, Claudia  
APPLICANT: Fry, George  
TITLE OF INVENTION: Multiplex Polynucleotide Capture  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PE Applied Biosystems  
STREET: 850 Lincoln Centre Drive  
CITY: Foster City  
STATE: CA  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873,437  
FILING DATE: 12-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,832  
FILING DATE: 04-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bortner, Scott R.  
REGISTRATION NUMBER: 34,298  
REFERENCE/DOCKET NUMBER: 4294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-638-6245  
TELEFAX: 415-638-6071  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-873-437-2

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTT 4488  
DB 1 TTTTGTCTT 25

RESULT 48  
US-09-197-951-5  
Sequence 5, Application US/09197951  
Patent No. 6197554  
GENERAL INFORMATION:  
APPLICANT: LIN, SHI-LUNG  
APPLICANT: CHUNG, CHENG-MING  
YING, SHAO-YAO  
TITLE OF INVENTION: Method for Generating Full-Length cDNA  
Library from Single Cells  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David & Raymond Patent Firm

STREET: 108 N. Ynez Ave., Suite 128  
CITY: Monterey Park  
STATE: CA  
COUNTRY: USA  
ZIP: 91754

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,951  
FILING DATE: 20-NO. 6197554-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chan, Raymond Y.C.  
REGISTRATION NUMBER: 37,484  
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 571-9812  
TELEFAX: (626) 571-9813  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic"  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-197-951-5

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTT 4488  
DB 1 TTTTGTCTT 25

RESULT 49  
US-09-522-217-38  
Sequence 38, Application US/09522217  
Patent No. 6307024  
GENERAL INFORMATION:  
APPLICANT: Premeil, Scott R.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Foster, Donald C.  
APPLICANT: Holly, Richard D.  
APPLICANT: Gross, Jane A.  
APPLICANT: Johnston, Janet V.  
APPLICANT: Nelson, Andrew J.  
APPLICANT: Dillon, Stacey R.  
APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/522,217  
CURRENT FILING DATE: 2000-03-09  
EARLIER APPLICATION NUMBER: US 60/123,547  
EARLIER FILING DATE: 1999-03-09  
EARLIER APPLICATION NUMBER: US 60/123,904  
EARLIER FILING DATE: 1999-03-11  
EARLIER APPLICATION NUMBER: US 60/142,013  
EARLIER FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 38  
LENGTH: 26  
TYPE: DNA





```
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38
```

```
Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25
```

```
RESULT 57
US-10-295-723-39
; Sequence 39, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald D.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-10-295-723-39
```

```
Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25
```

```
RESULT 58
US-08-208-486-79/c
; Sequence 79, Application US/08208486
; Patent No. 5389531
; GENERAL INFORMATION:
; APPLICANT: Ito, Junetsu
; APPLICANT: Yoo, Seung-Ku
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING
; TITLE OF INVENTION: PRD1-CATALYZED DNA REPLICATION SYSTEMS
; NUMBER OF SEQUENCES: 89
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cahill, Sulton & Thomas
; STREET: 155 Park One, 2141 E. Highland Ave.
; CITY: Phoenix
; STATE: Arizona
; COUNTRY: U.S.A.
; ZIP: 85016
```

## COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: Packard Bell (IBM PC/AT compatible)
; OPERATING SYSTEM: MS-Dos, Version 5.0
; SOFTWARE: WordPerfect Version 5.1
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,486
```

```
; FILING DATE:
```

```
; CLASSIFICATION: 435
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 07/869,916
```

```
; FILING DATE: April 14, 1992
```

```
; APPLICATION NUMBER: Japan 240525/91
```

```
; FILING DATE: August 26, 1991
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Janellie Faunce Raupp
```

```
; REGISTRATION NUMBER: 30,485
```

```
; REFERENCE/DOCKET NUMBER: #3954-A-7
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (602) 956-7000
```

```
; TELEFAX: (602) 495-9475
```

```
; INFORMATION FOR SEQ ID NO: 79:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 27 base pairs
```

```
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
```

```
US-08-208-486-79
```

```
Query Match          0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4464 TTTTGTGCTT 4488
Db      27 TTTTGTGCTT 3
```

```
RESULT 59
US-09-475-947A-153
; Sequence 153, Application US/09475947A
; Patent No. 6472154
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Garner, Harold R.
```

```
; APPLICANT: Wren, Jonathan D.
```

```
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
```

```
; FILE REFERENCE: UTSD0667
```

```
; CURRENT APPLICATION NUMBER: US/09/475,947A
```

```
; CURRENT FILING DATE: 1999-12-31
```

```
; NUMBER OF SEQ ID NOS: 346
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 153
```

```
; LENGTH: 27
```

```
; TYPE: DNA
```

```
; ORGANISM: human
```

```
US-09-475-947A-153
```

```
Query Match          0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4464 TTTTGTGCTT 4488
Db      2 TTTTGTGCTT 26
```



```

RESULT 60
US-08-433-505-9/c
: Sequence 9, Application US/08433505
: Patent No. 5695936
: GENERAL INFORMATION:
: APPLICANT: MANDRAND, Bernard
: APPLICANT: CROS, Philippe
: APPLICANT: DELAIR, Thierry
: APPLICANT: CHARLES, Marie-Helene
: APPLICANT: BROUT, Marie-No. 569593611e
: APPLICANT: PICHOT, Christian
: APPLICANT: TONNELIER, Jean-Claude
: TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
: TITLE OF INVENTION: A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OLIFP & BERRIDGE
: STREET: P.O. Box 19928
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/433,505
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BERRIDGE, WILLIAM P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: WPB 36349
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6400
: TELEFAX: 703-836-2787
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-433-505-9

Query Match 0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT GCTT 4488
|||||
Db 30 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 6.

RESULT 61
US-08-870-730-9/c
: Sequence 9, Application US/08870730
: Patent No. 6017707
: GENERAL INFORMATION:
: APPLICANT: MANDRAND, Bernard
: APPLICANT: CROS, Philippe
: APPLICANT: DELAIR, Thierry
: APPLICANT: CHARLES, Marie-Helene
: APPLICANT: BROUT, Marie-No. 601770711e
: APPLICANT: PICHOT, Christian
: TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
: TITLE OF INVENTION: A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:

```

QY	DB	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232
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RESULT 63
US-09-083-123-7/c
; Sequence 7, Application US/09083123
; Patent No. 6326143
; GENERAL INFORMATION:
; APPLICANT: Orum, Hendrik
; APPLICANT: Seeger, Corina
; TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
; FILE REFERENCE: Acids
; CURRENT APPLICATION NUMBER: US/09/083,123
; CURRENT FILING DATE: 1998-05-22
; EARLIER APPLICATION NUMBER: EP 95118600.6
; EARLIER FILING DATE: 1995-11-25
; EARLIER APPLICATION NUMBER: PCT/EP96/05149
; EARLIER FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-7
Query Match          0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred.No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      4464 TTTTGTGCTT 4488
Db      30 TTTTTTTTTTTTTTTTTT 6

RESULT 64
US-08-882-649A-10/C
; Sequence 10, Application US/0882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; CHEE, MARK
; Gunderson, Kevin
; Chaogiang, Lai
; Wodicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; McCall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-5834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,649A
; FILING DATE: 25-Jun-1997
; CLASSIFICATION: 435-006.000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,471
; FILING DATE: 23-JAN-1996

```

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; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US77/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; FEATURES:
; (ix) Features:
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-882-649A-10

Query Match          0.3%; Score 21.6; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTGTCTT 4488
       |||||
Db       30 TTTTTTTTTTTTTTTTTTTT 6

RESULT 65
US-09-648-040-4/c
; Sequence 4, Application US/09648040
; Patent No. 6436665
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/09/648,040
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,261
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4

Query Match          0.3%; Score 21.6; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      4460 GGACTTTTTTTTTTTTGTCTT 4488
       |||||
Db       30 GGTTTTTTTTTTTTTTTTTTTT 2

RESULT 66
US-09-475-947A-134
; Sequence 134, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
```

APPLICANT: Wren, Jonathan D.  
APPLICANT: Minna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
FILE REFERENCE: UTS0667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 134  
LENGTH: 24  
TYPE: DNA  
ORGANISM: human  
US-09-475-947A-134

Query Match 0.3%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGTC 4486  
Db 2 TTTTGTCTGTC 24

RESULT 67  
US-09-721-154-4  
Sequence 4, Application US/09721154  
Patent No. 6651008  
GENERAL INFORMATION:  
APPLICANT: Valdeberg, Eugeni  
APPLICANT: Adams, Cynthia  
APPLICANT: Sabry, James  
APPLICANT: Crompton, Anne  
TITLE OF INVENTION: Database system including computer code  
FILE REFERENCE: CYCOP007C2  
CURRENT APPLICATION NUMBER: US/09/721,154  
CURRENT FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 09/311,996  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Paused-sequence  
US-09-721-154-4

Query Match 0.3%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4463 CTTTGTCTGTC 4485  
Db 1 CTTTGTCTGTC 23

RESULT 68  
US-08-910-632-5/c  
Sequence 5, Application US/08910632B  
Patent No. 6077668  
GENERAL INFORMATION:  
APPLICANT: KOOL, ERIC T.  
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES  
FILE REFERENCE: 220.0001030  
CURRENT APPLICATION NUMBER: US/08/910,632B  
CURRENT FILING DATE: 1997-08-13  
EARLIER APPLICATION NUMBER: 08/805,631  
EARLIER FILING DATE: 1997-02-26  
EARLIER APPLICATION NUMBER: 08/393,439  
EARLIER FILING DATE: 1995-02-23  
EARLIER APPLICATION NUMBER: 08/047,860

EARLIER FILING DATE: 1993-04-15  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic AS83 DNA nanocircle  
US-08-910-632-5

Query Match 0.3%; Score 21.2; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.7e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGTC 4489  
Db 26 TTTTGTCTGTC 1

RESULT 69  
US-08-805-631A-5/c  
Sequence 5, Application US/08805631A  
Patent No. 6096880  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF ROCHESTER  
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND  
FILE REFERENCE: DNA  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MUETING, RASCH & GEBHARDT, P.A.  
STREET: 119 No. 6096880th Fourth Street, Suite 201  
CITY: Minneapolis  
STATE: Minnesota  
COUNTRY: USA  
ZIP: 55401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/805,631A  
FILING DATE: 26-FEB-97  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,439  
FILING DATE: 23-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/047,860  
FILING DATE: 15-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SANDBERG, VICTORIA A.  
REGISTRATION NUMBER: 41,287  
REFERENCE/DOCKET NUMBER: 220.00010140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1226  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-805-631A-5

Query Match 0.3%; Score 21.2; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.7e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGTC 4489  
Db 1 TTTTGTCTGTC 1

Db 26 TTTT TTTT TTTT G TTTT TTTT TTTT G 1

RESULT 70  
US-09-569-344-5/c  
; Sequence 5, Application US/09569344  
; Patent No. 6368802  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF ROCHESTER  
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND  
; DNA  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEETING, RAASCH & GEBHARDT, P.A.  
; STREET: 119 No. 6368802th Fourth Street, Suite 201  
; CITY: Minneapolis  
; STATE: Minnesota  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/569,344  
; FILING DATE: 11-May-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/805,631  
; FILING DATE: 26-FEB-97  
; APPLICATION NUMBER: US 08/393,439  
; FILING DATE: 23-FEB-1995  
; APPLICATION NUMBER: US 08/047,860  
; FILING DATE: 15-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDBERG, VICTORIA A.  
; REGISTRATION NUMBER: 41,287  
; REFERENCE/DOCKET NUMBER: 220.00010140  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1226  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-569-344-5

Query Match 0.3%; Score 21.2; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.7e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT G TCTG 4469  
Db 26 TTTT TTTT TTTT G TTTT TTTT TTTT G 1

RESULT 71  
US-09-304-232-152  
; Sequence 152, Application US/09304232  
; Patent No. 6525185  
; GENERAL INFORMATION:  
; APPLICANT: Fan, Jian Bing  
; APPLICANT: Chakravarti, Aravinda  
; APPLICANT: Halushka, Marc Kenneth  
; APPLICANT: Case Western Reserve University School of Medicine  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Polymorphisms Associated With  
; TITLE OF INVENTION: Hypermethylation

FILE REFERENCE: 018547-034210US  
; CURRENT APPLICATION NUMBER: US/09/304,232  
; CURRENT FILING DATE: 1999-05-03  
; EARLIER APPLICATION NUMBER: US 60/084,641  
; EARLIER FILING DATE: 1998-05-07  
; NUMBER OF SEQ ID NOS: 909  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 152  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: APOA4 3058  
US-09-304-232-152

Query Match 0.3%; Score 21.2; DB 1; Length 29;  
Best Local Similarity 82.1%; Pred. No. 2.1e+02;  
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7405 AGCAACATCAGCAGCAGCAGCAGCA 7432  
Db 2 AGCAGAGACGACGACGAGCAGCAGCA 29

RESULT 72  
PCT-US92-10792-1  
; Sequence 1, Application PC/TUS9210792  
; GENERAL INFORMATION:  
; APPLICANT: Jayasena, Sumedha D.  
; APPLICANT: Johnston, Brian H.  
; TITLE OF INVENTION: Triplet Helix Formation at  
; TITLE OF INVENTION: (PunPyn)-(PunPyn) Tracts  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SRI International  
; STREET: 333 Ravenswood Avenue  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10792  
; FILING DATE: 19921211  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/826,934  
; FILING DATE: 21-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,452  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fabian, Gary R.  
; REGISTRATION NUMBER: 33,875  
; REFERENCE/DOCKET NUMBER: P-3141  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 859-4550  
; TELEFAX: (415) 859-3880  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: OLIGONUCLEOTIDE I, FIGURE 8  
PCT-US92-10792-1



REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-40

Query Match 0.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No.1.1e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7414 AGCAGCAGCAGCAGCAGCAGC 7434  
DB 1 GCAGCAGCAGCAGCAGCAGCAGC 21

RESULT 76  
US-08-863-639A-60/c  
Sequence 60, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Max  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-60

Query Match 0.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No.1.1e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433  
DB 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 77  
US-08-863-639A-66  
Sequence 66, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Max  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-66

Query Match 0.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No.1.1e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCAGCA 7435  
DB 1 GCAGCAGCAGCAGCAGCAGCA 21

RESULT 78  
US-08-863-639A-69/c  
Sequence 69, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Max  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

```

;
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-69

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7414 AGCAGCAGCAGCAGCAGCAGC 7434
Db      21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 79
US-08-863-639A-87/c
; Sequence 87, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coasain, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
```

```

US-08-863-639A-87

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7415 GCAGCAGCAGCAGCAGCAGCA 7435
Db      21 GCAGCAGCAGCAGCAGCAGCA 1

RESULT 80
US-08-400-275-13
; Sequence 13, Application US/08400275
; Patent No. 5668295
; GENERAL INFORMATION:
; APPLICANT: Wahab, Samir Z.
; APPLICANT: Malik, Vedpal S.
; TITLE OF INVENTION: PUTRESCINE N-METHYLTRANSFERASE.
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING PUTRESCINE
; TITLE OF INVENTION: N-METHYLTRANSFERASE, AND TRANSGENIC TOBACCO PLANTS WITH
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Ave. of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,275
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,681
; FILING DATE:
; APPLICATION NUMBER: US 07/613,160
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: PM-1696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-400-275-13

Query Match          0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTCTTTCTTTCTTTCTTTCTTTT 4483
Db      9 CTTTCTTTCTTTCTTTCTTTCTTT 29

RESULT 81
US-08-227-476-5/c
```

```
; Sequence 5, Application US/08227476
; Patent No. 6498025
; GENERAL INFORMATION:
; APPLICANT: Miller, Jeffrey E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR cDNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray, Cary, Ames & Frye
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,851
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weseman, James C.
; REGISTRATION NUMBER: 39,507
; REFERENCE/DOCKET NUMBER: P0023US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3604
; TELEFAX: (619) 236-1048
; TELEX: 910-335-1273
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-227-476-5

Query Match          0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      21 CTTTTTTTTTTTTTTTTTTT 1

RESULT 82
US-09-475-947A-332
; Sequence 332, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 332
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-332

Query Match          0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.5e+02;
```

```
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      52 GCGCGAAGGAGCTGCGGGCGCGCG 80
Db      1 GCGGCGGCGCGCGCGCGCGCGCGG 29

RESULT 83
US-08-522-623-14
; Sequence 14, Application US/08522623
; Patent No. 5585242
; GENERAL INFORMATION:
; APPLICANT: Khalil, Omar S.
; APPLICANT: Bouma, Stanley R.
; APPLICANT: Pabich, Edward K.
; TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,839
; FILING DATE:
; APPLICATION NUMBER: US/07/863,553
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brainard, Thomas D.
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5158.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-4864
; TELEFAX: (708) 937-9556
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 32
US-08-522-623-14

Query Match          0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      12 CTTTTTTTTTTTTTTTTTTT 32

RESULT 84
US-09-619-103-14/C
; Sequence 14, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
```



APPLICANT: Lohse, Peter  
APPLICANT: Wagner, Richard  
TITLE OF INVENTION: Peptide Acceptor Ligation Methods  
FILE REFERENCE: 50036/031002  
CURRENT APPLICATION NUMBER: US/09/619,103  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 60/145,834  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 32  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: designed sequence to act as a linker  
US-09-619-103-14

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT G 4484  
|||||  
Db 30 TTTT TTTT TTTT TTTT TTTT TTTT G 10

RESULT 85  
PCT-US93-03256-14  
Sequence 14, Application PC/TUS9303256  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF  
NUMBER OF SEQUENCES: 14  
TITLE OF INVENTION: NUCLEIC ACID OR ANALYTE USING TOTAL INTERNAL REFLECTION  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: One Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn and WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03256  
FILING DATE: 19930506  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/863,553  
FILING DATE: 06 April 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Brainard, Thomas D.  
REGISTRATION NUMBER: 32,459  
REFERENCE/DOCKET NUMBER: 5158, US, 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 937-2623  
TELEFAX: (708) 937-4884  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 32  
PCT-US93-03256-14

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4463 CTTT TTTT TTTT TTTT TTTT TTTT T 4483  
|||||  
Db 12 CTTT TTTT TTTT TTTT TTTT TTTT T 32

RESULT 86  
US-08-014-943A-25/c  
Sequence 25, Application US/08014943A  
Patent No. 5545551  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergmann, Andrew D.  
TITLE OF INVENTION: Cloning And Expression Of PUR Protein  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,943A  
FILING DATE: 02/FEB/1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TEXT: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-25

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT GCT 4487  
|||||  
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT T 1

RESULT 87  
US-08-486-421-50/c  
Sequence 50, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergmann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York

```
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-421-50
```

```
Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTTTGTCT 4487
Db 24 TTTTGTCTTTTGTCTTTT 1
```

```
RESULT 88
US-08-470-911-50/c
Sequence 50. Application US/08470911
Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
```

```
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-470-911-50
```

```
Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4464 TTTTGTCTTTTGTCT 4487
Db 24 TTTTGTCTTTTGTCTTTT 1
```

```
RESULT 89
US-08-735-381-1/c
Sequence 1. Application US/08735381
Patent No. 5853993
GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
APPLICANT: Dahm, SueAnn
APPLICANT: Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
ADDRESSEE: Intellectual Property
STREET: 1501 Page Mill Road, MS 4U-10
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,381
FILING DATE: 21-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10950427-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-735-381-1
```

```
Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4464 TTTTGTCTTTTGTCT 4487
Db 24 TTTTGTCTTTTGTCTTTT 1
```

```

US-08-486-809-50/c
; Sequence 50, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486, 809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9030
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-486-809-50

Query Match          0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      4464 TTTTGTGCT 4487
         |||||
Db      24 TTTTTTTTTTTTTTTTTT 1

RESULT 91
US-09-183-619-7/c
; Sequence 7, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
; APPLICANT: DELINGER, DOUGLAS J.
; APPLICANT: DAHM, SUEANN C.
; APPLICANT: LISLEY, DIANE D.
; APPLICANT: ACH, ROBERT A.
; APPLICANT: TROLL, MARK A.
; TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
; FILE REFERENCE: 10981619-1
; CURRENT APPLICATION NUMBER: US/09/183,619
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 08/735,381
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 7
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: poly A-RNA target
US-09-183-619-7

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTT TTTTTTTTTTTTTTGCTC 4487
          |||||
Db       24 TTTT TTTTTTTTTTTTTTTTTT 1

RESULT 92
US-09-201-674-1/C
; Sequence 1, Application US/09201674
; Patent No. 6110682
; GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
           Dahm, SueAnn
           Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Hewlett-Packard Company, Legal Dept.,
        Intellectual Property
        Street: 1501 Page Mill Road, MS 4U-10
        City: Palo Alto
        State: California
        Country: USA
        ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201.674
FILING DATE: 30-No. 6110682-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,381
FILING DATE: 21-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10950427-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-201-674-1

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY . 4464 TTTT TTTTTTTTTTTTTTGCTC 4487

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Db 24 |||||  
 TTTT

RESULT 93  
 US-09-536-936-11/c  
 ; Sequence 11, Application US/09536936  
 ; Patent No. 6346384  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pollner, Reinhold  
 ; TITLE OF INVENTION: Real Time Monitoring of PCR Using LOCI  
 ; FILE REFERENCE: BEH-7438  
 ; CURRENT APPLICATION NUMBER: US/09/536,936  
 ; CURRENT FILING DATE: 2001-06-11  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 11  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; OTHER INFORMATION: Oligonucleotide attached to beads  
 US-09-536-936-11

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 1.7e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT  
 Db 24 TTTT

RESULT 94  
 US-09-025-639-4/c  
 ; Sequence 4, Application US/09025639  
 ; Patent No. 6365346  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kurn, Nurith  
 ; APPLICANT: Patel, Rajesh D.  
 ; TITLE OF INVENTION: Quantitative Determination of Nucleic  
 ; FILE REFERENCE: BEH-7408  
 ; CURRENT APPLICATION NUMBER: US/09/025,639  
 ; CURRENT FILING DATE: 1998-02-18  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc\_binding  
 ; LOCATION: (1)..(24)  
 ; OTHER INFORMATION: Synthetic DNA Probe  
 US-09-025-639-4

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 1.7e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT  
 Db 24 TTTT

RESULT 95  
 US-09-333-237-4/c  
 ; Sequence 4, Application US/09333237  
 ; Patent No. 6406667  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Singh, Sharat  
 ; APPLICANT: Ullman, Edwin F.

; TITLE OF INVENTION: Chemiluminescent Compositions For Use In  
 ; TITLE OF INVENTION: Detection Of Multiple Analyses  
 ; FILE REFERENCE: BEH-7383A  
 ; CURRENT APPLICATION NUMBER: US/09/333,237  
 ; CURRENT FILING DATE: 1999-06-15  
 ; PRIOR APPLICATION NUMBER: 09/025,624  
 ; PRIOR FILING DATE: 1998-02-18  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: detection probe bound to sensitizer particle  
 US-09-333-237-4

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 1.7e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT  
 Db 24 TTTT

RESULT 96  
 US-09-732-067-1/c  
 ; Sequence 1, Application US/09732067  
 ; Patent No. 6457426  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ullman, Edwin  
 ; APPLICANT: Dekeszer, Steve  
 ; APPLICANT: Davalian, Darlush  
 ; TITLE OF INVENTION: Amplified Luminescent Homogeneous  
 ; FILE REFERENCE: BEH-7385  
 ; CURRENT APPLICATION NUMBER: US/09/732,067  
 ; CURRENT FILING DATE: 2000-12-07  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: hybridization oligo  
 US-09-732-067-1

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 1.7e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT  
 Db 24 TTTT

RESULT 97  
 US-10-043-415-4/c  
 ; Sequence 4, Application US/10043415  
 ; Patent No. 6573054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kurn, Nurith  
 ; APPLICANT: Patel, Rajesh D.  
 ; TITLE OF INVENTION: Quantitative Determination of Nucleic  
 ; FILE REFERENCE: BEH-7408  
 ; CURRENT APPLICATION NUMBER: US/10/043,415  
 ; CURRENT FILING DATE: 2002-01-10  
 ; PRIOR APPLICATION NUMBER: US/09/025,639  
 ; PRIOR FILING DATE: 1998-02-18

```

: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 3.0.
: SEQ ID NO 4
: LENGTH: 24
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: misc_binding
: LOCATION: (1)...(24)
: OTHER INFORMATION: Synthetic DNA Probe
US-10-043-415-4

```

```
Query Match#      0.3%; Score 20.8; DB 1; length 24;
Best local similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Indels 0; Gaps 0;
```

```
QY      4464 TTTTTTTTTTTTTTTTGGCT 4487
          |||||
Db       24 TTTTTTTTTTTTTTTT 1
```

RESULT 98  
 US-09-854-317-1/c  
 : Sequence 1, Application US/09854317  
 : Patent No. 6582938  
 : GENERAL INFORMATION:  
 : APPLICANT: Su, Xing  
 : APPLICANT: Dong, Heli  
 : APPLICANT: Ryder, Thomas B.  
 : TITLE OF INVENTION: Amplification of Nucleic Acids  
 : FILE REFERENCE: 3234.2  
 : CURRENT APPLICATION NUMBER: US/09/854,317  
 : CURRENT FILING DATE: 2001-05-11  
 : NUMBER OF SEQ ID NOS: 5  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 1  
 : LENGTH: 24  
 : TYPE: DNA  
 : ORGANISM: artificial sequence  
 : FEATURE:  
 : OTHER INFORMATION: synthetic oligonucleotide  
 : US-09-854-317-1

Query Match	0.3%	Score 20.8;	DB 1;	Length 24;
Best Local Similarity	91.7%;	Pred. No. 1.7e+02;		
Matches	22;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

```
QY      4464 TTTTTTTTTTTTTTTTTTGTCT 4487
          |||||
Db      24  TTTTTTTTTTTTTTTTTTTT 1
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```

1 RESULT 99
2 US-09-721-154-1
3
4 : Sequence 1, Application US/09721154
5 : Patent No. 6651008
6 :
7 : GENERAL INFORMATION:
8 :
9 : APPLICANT: Valdsberg, Eugeni
10 : APPLICANT: Adams, Cynthia
11 : APPLICANT: Sabry, James
12 : APPLICANT: Crompton, Anne
13 :
14 : TITLE OF INVENTION: Database system including computer code
15 : TITLE OF INVENTION: for predictive cellular bioinformatics
16 :
17 : FILE REFERENCE: CYP0070762
18 :
19 : CURRENT APPLICATION NUMBER: US/09/721,154
20 :
21 : PRIOR FILING DATE: 2002-06-14
22 : PRIOR APPLICATION NUMBER: 09/311,996
23 :
24 : NUMBER OF SEQ ID NOS: 14
25 :
26 : SOFTWARE: FASTSEQ for Windows Version 4.0
27 :
28 : SEQ ID NO 1
29 :
30 : LENGTH: 24
31 :
32 : TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Pseudo-sequence
US-09-721-154-1

```

Query Match	0.3%	Score	20.8	DB 1	Length	24			
Best Local Similarity	91.7%	Pred. No.	1.7e+02						
Matches	22	Conservative	0	Mismatches	2	Indels	0	Gaps	0

```
QY      4465 TTTTTTTTTTTTTTTTGCTT 4488
          |||||
Db       1 TTTTTTTTTTTTTTTATT 24
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RESULT 100  
US-08-784-208-3  
; Sequence 3, Application US/08784208

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```

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 222/167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-784-208-3

Query Match	0.3%	Score	20.8	DB	1	Length	32
Best Local Similarity	78.1%	Pred. No.	3.1e+02				
Matches	25	Conservative	0	Mismatches	7	Indels	0
						Gaps	0

```

Qy      4465 TTTTTTTTTTTTTTTTTTGTCTGAGACATG 4496
          |||||
Db       1 TTTTTTTTTTTTTTTTCGCCGCGCATG 32

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RESULT 101  
US-08-123-449A-19/c

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; Sequence 19; Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:
; APPLICANT: TORENCCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEANING SPECIFIC SEQUENCES
; NUMBER OF INVENTION: OF RNA      22
; ADDRESSSEE: Knobb, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 1-4
; OTHER INFORMATION: A is linked by 2',5'-linkage
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 4
; OTHER INFORMATION: A is linked at 2' end to following
; OTHER INFORMATION: Base through a linker moiety
; US-08-133-449A-19
Query Match          0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No.1.7e+02;
Matches    21; Conservative   0; Mismatches     1; Indels       0; Gaps        0;
Q#         4464 TTTTTTTTTTTTTTTTGT 4485
Db          22 TTTTTTTTTTTTTTTTTT 1
```

```

APPLICANT: RATAN, MAITRA
TITLE OF INVENTION: METHOD OF CLEANING SPECIFIC SEQUENCES
TITLE OF INVENTION: METHOD OF CLEANING SPECIFIC SEQUENCES
NUMBER OF INVENTION: OF RNA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,050
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,449
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: PCT/US93/10103
FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH034,001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: miscellaneous feature
LOCATION: 1-4
OTHER INFORMATION: A is linked by 2',5'-linkage
NAME/KEY: miscellaneous feature
LOCATION: 4
OTHER INFORMATION: A is linked at 2' end to following
OTHER INFORMATION: base through a linker moiety
US-08-458-050-19

Query Match          0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464 TTTT TTTTTTTTTTTTTTTGCT 4485
Db       22 TTTT TTTTTTTTTTTTTTTT 1

RESULT 103
US-08-847-844A-94/C
Sequence 94, Application US/08847844A
Patent No. 6150160
GENERAL INFORMATION:
APPLICANT: KAZAZIAN JR., HAIG H.
APPLICANT: BOEKE, JEF D.
APPLICANT: MORAN, JOHN V.
APPLICANT: DOMEROSKI, BETH A.
```



```
; OTHER INFORMATION: Description of Artificial Sequence: Poly A
; OTHER INFORMATION: nucleotide sequence
US-09-720-201A-25

Query Match          0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4485
DB 22 TTTTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 106
US-09-721-154-6
; Sequence 6, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugene
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; TITLE OF INVENTION: for predictive cellular bioinformatics
; FILE REFERENCE: Cyto007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pseudo-sequence
US-09-721-154-6

Query Match          0.3%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTGTGTGTGTGTGTGTGTGT 4488
DB 2 TTTTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 107
US-08-117-361C-3
; Sequence 3, Application US/08117361C
; Patent No. 5773223
; GENERAL INFORMATION:
; APPLICANT: Venkatakrishna, Shyamala
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: Endocheilin B1 (ETB1) Receptor Polypeptide
; TITLE OF INVENTION: Compositions, Methods, and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 946087
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,361C
```

```
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 0945.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-117-361C-3

Query Match          0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4460 GACCTTTTGTGTGTGTGTGTGTGTGT 4481
DB 5 GACCTTTTGTGTGTGTGTGTGTGTGT 26

RESULT 108
US-08-666-405-15
; Sequence 15, Application US/0866405
; Patent No. 5874220
; GENERAL INFORMATION:
; APPLICANT: FACH, Patrick; GUILLOU,
; APPLICANT: Jean-Pierre; POPOFF, Michel
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: AMPLIFICATION OF GENES CODING FOR THE
; TITLE OF INVENTION: ENTEROTOXIN AND THE LECTININASE OF CLOSTRIDIUM
; TITLE OF INVENTION: PERFRINGENS AND THEIR APPLICATION TO THE
; TITLE OF INVENTION: DETECTION AND NUMERATION OF THESE BACTERIAE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,405
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04292
; FILING DATE: 22-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/172,026
; FILING DATE: 22-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 102.164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
```



STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Clostridium perfringens  
US-08-666-405-15

Query Match	0.3%	Score	20.2	DB	1	Length	29
Best Local Similarity	88.0%	Score	No.3.3e+02				
Matches	22	Conservative	0	Mismatches	3	Indels	0
						Gaps	0

```
QY      4460 GGACTTTT TTTT TTTT TTTT TG 4484
          ||| |||| | |||| |||| |||
Db       2   GGAGTTTT TATT TTTT TTTT TG 26
```

```

RESULT 109
US-08-910-632-6
; Sequence 6, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220, 00010130
; CURRENT APPLICATION NUMBER: US/08/910, 632B
; CURRENT FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805, 631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393, 439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047, 860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multimer
US-08-910-632-6

```

Query Match	0.3%	Score 20.2;	DB 1;	Length 29;
Best Local Similarity	88.0%	Pred. No. 3.3e+02;		
Matches 22;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	4464	TTTTTTTTTTTTTTTTTTGTCCT	4488
Db	5	TTTTTTTTTTTTTTGTTTTTTTTT	29

```

RESULT 110
US-08-805-631A-6
; Sequence 6, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA ANT
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NO. 6096880th Fourth Street, Suite 201
; City: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

1  APPLICATION NUMBER:  US/08/805,631A
2  FILING DATE:  26-FEB-97
3  CLASSIFICATION:  536
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER:  US 08/393,439
6  FILING DATE:  23-FEB-1995
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER:  US 08/047,860
9  FILING DATE:  15-APR-1993
10 ATTORNEY/AGENT INFORMATION:
11 NAME:  SANDBERG, VICTORIA A.
12 REGISTRATION NUMBER:  41,287
13 REFERENCE/DOCKET NUMBER:  220.00010140
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE:  612-305-1226
16 TELEFAX:  612-305-1228
17 INFORMATION FOR SEQ ID NO:  6:
18     SEQUENCE CHARACTERISTICS:
19         LENGTH:  29 base pairs
20         TYPE:  nucleic acid
21         STRANDEDNESS:  single
22         TOPOLOGY:  linear
23     MOLECULE TYPE:  DNA (genomic)
24     US-08-631A-6

```

Query Match	0.3%	Score	20.2	DB 1	Length	29			
Best Local Similarity	88.0%	Pred. No.	3.3e+02						
Matches	22	Conservative	0	Mismatches	3	Indels	0	Gaps	0

Qy 4464 TTTTTTTTTTTTTTTTTTGTCTT 4488  
 Db 5 TTTTTTTTTTTGTTTTTTTTTTT 29

RESULT 111  
 : Sequence 6, Application US/09569344-6  
 : Patent No. 6368602  
 : GENERAL INFORMATION:  
 : APPLICANT: UNIVERSITY OF ROCHESTER  
 : TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA ANT  
 : DNA  
 : NUMBER OF SEQUENCES: 72  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MOETING, RAASCH & GEBHARDT, P.A.  
 : STREET: 119 No. 6368602th Fourth Street, Suite 201  
 : CITY: Minneapolis  
 : STATE: Minnesota  
 : COUNTRY: USA  
 : ZIP: 55401  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/569,344  
 : FILING DATE: 11-May-2000  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/805,631  
 : FILING DATE: 26-FEB-97  
 : APPLICATION NUMBER: US 08/393,439  
 : FILING DATE: 23-FEB-1995  
 : APPLICATION NUMBER: US 08/047,860  
 : FILING DATE: 15-APR-1993  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SANDBERG, VICTORIA A.  
 : REGISTRATION NUMBER: 41,287  
 : REFERENCE/DOCKET NUMBER: 220.00010140  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 612-305-1226  
 : TELEFAX: 612-305-1228

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 29 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-569-344-6

Query Match      0.3%; Score 20.2; DB 1; Length 29;
Best Local Similarity 88.0%; Pred. No. 3.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4464 TTTTGTGTTTGTGTTTGTGTTT 4488
DB      5 TTTTGTGTTTGTGTTTGTGTTT 29

RESULT 112
US-08-146-504-16
; Sequence 16, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
;   APPLICANT: Heller, Michael J.; and Tu, Eugene
;   TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
;   TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
;   TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 611 West Sixth Street
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90017
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;   SOFTWARE: Wordperfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/146,504
;   FILING DATE: No. 5605662member 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   PRIOR APPLICATION DATA: including application
;   PRIOR APPLICATION DATA: described below:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Warburg, Richard J.
;   REGISTRATION NUMBER: 32,327
;   REFERENCE/DOCKET NUMBER: 203/218
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 489-1600
;   TELEFAX: (213) 955-0440
;   TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   US-08-146-504-16

Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTGTGTTTGTGTTTGTGTTT 4483
DB      1 TTTTGTGTTTGTGTTTGTGTTT 20
```

```

DB      1 TTTTGTGTTTGTGTTTGTGTTT 20

RESULT 113
US-08-379-593-5
; Sequence 5, Application US/08379593
; Patent No. 5849480
; GENERAL INFORMATION:
;   APPLICANT: Cros, Philippe
;   APPLICANT: Kurfurst, Robin
;   APPLICANT: Battail, Nicole
;   APPLICANT: Piga, Nadia
;   TITLE OF INVENTION: HAPTEN ASSAY DEVICE AND USE THEREOF
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OLTF & BERRIDGE
;   STREET: 700 South Washington Street, Suite 300
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: USA
;   ZIP: 22314
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Floppy disk, 1.44M storage
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/379,593
;   FILING DATE: 02-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Berridge, William P.
;   REGISTRATION NUMBER: 30,024
;   REFERENCE/DOCKET NUMBER: WPP 36056
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6400
;   TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "SYNTHETIC DNA"
;   FEATURE:
;   OTHER INFORMATION: consists of nucleosides with an alpha anomer and carries
;   US-08-379-593-5

Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTGTGTTTGTGTTTGTGTTT 4483
DB      1 TTTTGTGTTTGTGTTTGTGTTT 20

RESULT 114
US-08-725-976-16
; Sequence 16, Application US/08725976
; Patent No. 5929208
; GENERAL INFORMATION:
;   APPLICANT: Heller, Michael J.; and Tu, Eugene
;   TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 633 West Fifth Street
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90071
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: WINDOWS (VERSION 3.0)  
SOFTWARE: WordPerfect (Version 6.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,976  
FILING DATE: October 4, 1996  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: described below:  
FILING DATE: No. 5929208ember 1, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, David B.  
REGISTRATION NUMBER: 31,125  
REFERENCE/DOCKET NUMBER: 222/211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-725-976-16

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 115  
US-08-997-080-83/c  
Sequence 83, Application US/08997080  
Patent No. 5968524  
GENERAL INFORMATION:  
APPLICANT: WATSON, JAMES D.  
APPLICANT: TAN, PAUL L.J.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
NUMBER OF SEQUENCES: 194  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,080  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleach, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563  
TEXT:  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
US-08-997-080-83

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 116  
US-08-997-362-83/c  
Sequence 83, Application US/08997362  
Patent No. 5985287  
GENERAL INFORMATION:  
APPLICANT: Tan, Paul  
APPLICANT: Hiya, Jun  
APPLICANT: Visser, Elizabeth  
APPLICANT: Skinner, Margot  
APPLICANT: Scott, Linda  
APPLICANT: Prestidge, Rose  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR  
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 194  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,362  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970  
FILING DATE: June 12, 1997  
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347  
FILING DATE: August 29, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleach, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1002c2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TEXT:  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
US-08-997-362-83

Query Match 0.3%; Score 20; DB 1; Length 20;





```

? CURRENT FILING DATE: 1999-02-12
? NUMBER OF SEQ. ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.1
? SEQ. ID NO. 1
? LENGTH: 20
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)-(19)
? OTHER INFORMATION: 2'-methoxyethoxy (MOE)
? OTHER INFORMATION: Description of Artificial Sequence: No. 6207a19a1
? OS-09-250-075-1

```

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	4464	1	20	4483
Db				

RESULT 123  
 US-09-173-936B-14  
 ; Sequence 14, Application US/09173936B  
 ; Patent No. 6238865  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhen, Huang; Szostak, Jack W.  
 ; TITLE OF INVENTION: A Simple and Efficient Method to Label and Modify 3'-  
 ; Terminal  
 ; of RNA Using DNA Polymerase and a Synthetic Template with D  
 ; Nucleotides

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cohen, Pontani, Lieberman  
STREET: 551 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10176  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.50 inch Diskette  
COMPUTER: IBM-MS  
OPERATING SYSTEM: Window 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/173,936B  
FILING DATE: 16-Oct-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/063,757  
FILING DATE: 17-Oct-1997  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

[illegible]

```

RESULT 124
US-09-454-704A-13/c
Sequence 13, Application US/09454704A
Patent No. 6274321
GENERAL INFORMATION:
APPLICANT: Blumberg, Bruce
TITLE OF INVENTION: High Throughput Functional Screening of
FILE REFERENCE: P-UC 3662
CURRENT APPLICATION NUMBER: US/09/454,704A
CURRENT FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: cDNA
US-09-454-704A-13

```

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	4464	TTTTTTTTTTTTTTTTTTTT	4483
Db	20	TTTTTTTTTTTTTTTTTTTT	1

```

RESULT 125
US-09-324-542-83/c
? Sequence 83, Application US/09324542
? Patent No. 6328978
? GENERAL INFORMATION:
? APPLICANT: Watson, James D.
? APPLICANT: Tan, Paul L.J.
? APPLICANT: Prestidge, Ross
? TITLE OF INVENTION: Methods and Compounds for the Treatment
? TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
? FILE REFERENCE: 11000.1007c1
? CURRENT APPLICATION NUMBER: US/09/324,542
? CURRENT FILING DATE: 1999-06-02
? EARLIER APPLICATION NUMBER: US 08/997,080
? EARLIER FILING DATE: 1997-12-23
? NUMBER OF SEQ ID NOS: 194
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 83
? LENGTH: 20
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Made in a lab
US-09-324-542-83

```

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.6e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	4464	TTTTTTTTTTTTTTTTTTTTTTTTTTT	4483
Dd	20	TTTTTTTTTTTTTTTTTTTTTTTTTTT	1

```

RESULT 126
US-09-205-426-83/c
; Sequence 83, Application US/09205426
; Patent No.6405704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

```

```

1 FILE REFERENCE: 11000.1002c4
2 CURRENT APPLICATION NUMBER: 09/09/205,426
3 CURRENT FILING DATE: 1998-12-04
4 EARLIER APPLICATION NUMBER: 09/0955,855
5 EARLIER FILING DATE: 1998-06-11
6 EARLIER APPLICATION NUMBER: 08/997,362
7 EARLIER FILING DATE: 1997-12-23
8 EARLIER APPLICATION NUMBER: 08/873,970
9 EARLIER FILING DATE: 1997-06-12
10 EARLIER APPLICATION NUMBER: 08/705,347
11 EARLIER FILING DATE: 1996-08-29
12 NUMBER OF SEQ ID NOS: 208
13 SOFTWARE: PasteSeq for Windows Version 3.0
14 SEQ ID NO 83
15 LENGTH: 20
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Made in a lab
20 US-09-205-426-83

```

```

1 Sequence 55, Application US/09976978A
2 Patent No. 6532097
3 GENERAL INFORMATION:
4 APPLICANT: Mirkin, Chad A.
5 APPLICANT: Letsinger, Robert L.
6 APPLICANT: Mucic, Robert C.
7 APPLICANT: Storhoff, James J.
8 APPLICANT: Elghanian, Robert
9 APPLICANT: Taton, Thomas A.
10 TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
11 FILE REFERENCE: 00-713-117
12 CURRENT APPLICATION NUMBER: US/09/976, 978A
13 CURRENT FILING DATE: 2002-03-05
14 PRIOR APPLICATION NUMBER: 09/603, 830
15 PRIOR FILING DATE: 2000-06-26
16 PRIOR APPLICATION NUMBER: 09/344, 667
17 PRIOR FILING DATE: 1999-06-25
18 PRIOR APPLICATION NUMBER: 09/240, 755
19 PRIOR FILING DATE: 1999-01-29
20 PRIOR APPLICATION NUMBER: PCT/US97/12783
21 PRIOR FILING DATE: 1997-07-21
22 PRIOR APPLICATION NUMBER: 60/031, 809
23 PRIOR FILING DATE: 1996-07-29
24 PRIOR APPLICATION NUMBER: 60/200, 161
25 PRIOR FILING DATE: 2000-04-26
26 NUMBER OF SEQ ID NOS: 64
27 SOFTWARE: Microsoft word 2000
28 SEQ ID NO 55
29 LENGTH: 20
30 TYPE: DNA
31 ORGANISM: Artificial Sequence
32 FEATURE:
33 OTHER INFORMATION: Description of Artificial Sequence:random
34 OTHER INFORMATION: synthetic sequence
35 US-09-976-978A-55

```

```
Query Match          0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity    100.0%; Pred.No. 1.ee+02;  
Matches      20; Conservative     0; Mismatches         0; Gaps       0;  
  
OY           4464 TTTTTTTTTTTTTTTT 4483  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
              |||  
Db            20 TTTTTTTTTTTTTTTTTT 1  
  
RESULT 131  
US-09-344-260A-10 US-09-344-260A-10  
Sequence 10, Application US/09344260A  
Patent No. 6576752  
GENERAL INFORMATION:  
APPLICANT: Manoharan, Muthiah  
APPLICANT: Lonnberg, Harri  
APPLICANT: Salo, Harri  
APPLICANT: Virta, Pasi  
TITLE OF INVENTION: Aminoxy Functionalized Oligomers  
FILE REFERENCE: ISIS-3508  
CURRENT APPLICATION NUMBER: US/09/344,260A  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 09/016,520  
PRIOR FILING DATE: 1998-01-30  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: No. 6576752el Sequence  
US-09-344-260A-10
```

0.3%; Score 20; DB 1; Length 20;

Pred.No. 1.ee+02;

Gaps 0;

```

Best Local Similarity 100.0%;  Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
    |||
Db 1 TTTTTTTTTTTTTTTTTT 20

```

```

RESULT 132
US-09-961-949A-55/c
/ Sequence 55, Application US/09961949A
/ Patent No. 6582921
/ GENERAL INFORMATION:
/ APPLICANT: Mirkin, Chad A.
/ APPLICANT: Letsinger, Robert L.
/ APPLICANT: Mucic, Robert C.
/ APPLICANT: Steinhoff, James J.
/ APPLICANT: Elghanian, Robert
/ APPLICANT: Taton, Thomas A.
/ TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
/ TITLE OF INVENTION: AND USES THEREFOR
/ FILE REFERENCE: 00-713-11
/ CURRENT APPLICATION NUMBER: US/09/961,949A
/ CURRENT FILING DATE: 2001-09-20
/ PRIOR APPLICATION NUMBER: 09/603,830
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: 09/344,667
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/240,755
/ PRIOR FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: PCT/US97/12783
/ PRIOR FILING DATE: 1997-07-21
/ PRIOR APPLICATION NUMBER: 60/031,809
/ PRIOR FILING DATE: 1996-07-29
/ PRIOR APPLICATION NUMBER: 60/200,161
/ PRIOR FILING DATE: 2000-04-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Microsoft word 2000
/ SEQ ID NO 55
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE: Description of Artificial Sequence:random
/ OTHER INFORMATION: synthetic sequence
US-09-961-949A-55

```

```

Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Gaps

QY      4464 TTTTTTTTTTTTTTTTTT 4483
          |||||
Db       20 TTTTTTTTTTTTTTTTTT 1

RESULT 133
US-09-966-491A-55/c
; Sequence 55, Application US/09966491A
; Patent No. 6610491
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THEREFOR
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-14
CURRENT APPLICATION NUMBER: US/09/966,491A
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/603,830

```





```

; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-062A-55
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4464 TTTT TTTT TTTT TTTT TTTT 4483
Db       20 TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 137
US-09-976-971A-55/c
; Sequence 55, Application US/09976971A
; Patent No. 6682895
; GENERAL INFORMATION:
; APPLICANT: Mitkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Steinhoff, James J.
; APPLICANT: Elghamian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND US$S THEREFOR
; FILE REFERENCE: 00-713-118
; CURRENT APPLICATION NUMBER: US/09/976,971A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-971A-55
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4464 TTTT TTTT TTTT TTTT TTTT 4483
```

```
Db       20 TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 138
PCT-US93-07603-6/c
; Sequence 6, Application PC/TUS9307603
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACID RECOGNITION AND TRANSPORT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07603
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,087
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0636/7007WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Synthetic RNA oligonucleotide.
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US93-07603-6
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4464 TTTT TTTT TTTT TTTT TTTT 4483
Db       20 TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 139
US-08-146-504-2/c
; Sequence 2, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
;
```

```
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,504
FILING DATE: No. 5605662ember 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-146-504-2

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 140
US-08-455-896-13
Sequence 13, Application US/08455896
Patent No. 5668267
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
NUMBER OF SEQUENCES: 13
REFERENCE/DOCKET NUMBER: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESS: ROGERS, HOWELL & HAFERRAMP
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
ZIP: 63105-1817
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,896
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 952726
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-455-896-13

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 141
US-08-933-149-13
Sequence 13, Application US/08933149
Patent No. 5922836
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: HOWELL & HAFERRAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
ZIP: 63105-1817
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,149
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HENDERSON, MELDIE W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-933-149-13

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
```

RESULT 142  
US-08-725-976-2/c  
Sequence 2, Application US/08725976  
Patent No. 5929208  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J. and Tu, Eugene  
TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 613 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: WINDOWS (VERSION 3.0)  
SOFTWARE: WordPerfect (Version 6.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,976  
FILING DATE: October 4, 1996  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/146,504  
FILING DATE: No. 5929208ember 1, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, David B.  
REGISTRATION NUMBER: 31,125  
REFERENCE/DOCKET NUMBER: 222/211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEFAX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-725-976-2

Query Match 0.3%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483  
|||||  
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 143  
US-09-082-343-13  
Sequence 13, Application US/09082343  
Patent No. 5968754  
GENERAL INFORMATION:  
APPLICANT: WATSON, MARK A.  
APPLICANT: FLEMING, TIMOTHY P.  
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105-1817

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/082,343  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/455,896  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 952726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-09-082-343-13

Query Match 0.3%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 144  
US-08-863-639A-10/c  
Sequence 10, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Watson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Muehl  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321